80520

184793

mg

STIC-Biotech/ChemLib

From: Bowman, Amy
Sent: Tuesday, April 11, 2006 6:04 AM
To: STIC-Biotech/ChemLib
Cc: Bowman, Amy
Subject: sequence search-10/728,399

CRF

Hello,
I need a score over length search of SEQ ID NO: 1 in application 10/728,399, with lower and upper limits of 8 and 30 nucleobases, respectively, and a minimum of 80% identity.
Thank you,
Amy Bowman
AU 1635
REM 2C31
mail REM 2C18
571-272-0755

Na 20

RECEIVED
APR 11 2006
STIC

mg

Deirdre Amour

****
Searcher:_____
Searcher Phone:_____
Date Searcher Picked up:_____
Date completed:_____
Searcher Prep Time:_____
Online Time:_____

****
Type of Search
NA#_____ AA#:_____
S/L:_____ Oligomer:_____
Encode/Transl:_____
Structure #:_____Text:____
Inventor:_____ Litigation:___

****
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____
Other (Specify):_____

THIS PAGE LEFT BL

4/24/06

10/728,399

SLD 1

SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 80%

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.

THIS PAGE LEFT BLANK

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 23, 2006, 11:43:23 ; Search time 0.001 Seconds
(without alignments)
47.800 Million cell updates/sec

Title: US-10-728-399-1
Perfect score: 20
Sequence: 1 ttgtctccagtctcttcgtt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 106 seqs, 1195 residues

Total number of hits satisfying chosen parameters: 212

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : rng.subdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	1	ADP69107	Human mitoNEET-spe
	2	19	95.0	20	1	ADP69109	Human mitoNEET-spe
	3	19	95.0	20	1	ADP69110	Human mitoNEET-spe
	4	18	90.0	20	1	ADP69108	Human mitoNEET-spe
	5	18	90.0	20	1	ADP69116	Human mitoNEET-spe
	6	17	85.0	20	1	ADP69124	Human mitoNEET-spe
	7	17	85.0	20	1	ADP69113	Human mitoNEET-spe
	8	16	80.0	20	1	ADP69111	Human mitoNEET-spe
	9	16	80.0	20	1	ADP69130	Human mitoNEET-spe
c	10	13.8	69.0	17	1	ABN09352	Human GDMLP-1 17-m
c	11	13.8	69.0	17	1	ABN09353	Human GDMLP-1 17-m
c	12	13.8	69.0	17	1	ABN09354	Human GDMLP-1 17-m
c	13	13.8	69.0	17	1	ACN72443	Human GDMLP-1 prob
c	14	13.8	69.0	17	1	ACN72442	Human GDMLP-1 prob
c	15	13.8	69.0	17	1	ACN72444	Human GDMLP-1 prob
c	16	10.4	52.0	13	1	ABF03676	Oligonucleotide SE
	17	10.4	52.0	13	1	ABF03677	Oligonucleotide SE
c	18	9.4	47.0	11	1	ABV64201	Human skin EST 198
c	19	9.4	47.0	11	1	ABV71622	Human skin EST 940
c	20	9.4	47.0	11	1	ADQ33489	Human facial skin-
c	21	9.4	47.0	11	1	ADQ32655	Human facial skin-
	22	9	45.0	10	1	AAZ81653	Metastatic breast
	23	9	45.0	10	1	AAF42075	Yeast NORF gene SA
c	24	9	45.0	10	1	ADU19570	Hypoxia-related tu
c	25	9	45.0	11	1	ABQ87397	Human skin stress/
c	26	9	45.0	11	1	ABV70379	Human skin EST 816
c	27	9	45.0	11	1	ABV62958	Human skin EST 744
	28	9	45.0	11	1	ABV69205	Human skin EST 699
	29	9	45.0	11	1	ABV66235	Human skin EST 402
c	30	9	45.0	11	1	ABV65400	Human skin EST 318
c	31	9	45.0	11	1	ADG64354	DNA polymerase 3'-
c	32	8.6	43.0	9	1	ADR36038	Human nicking agen
c	33	8.6	43.0	9	1	ADR36039	Human nicking agen
c	34	8.6	43.0	9	1	ADR36041	Human nicking agen
c	35	8.6	43.0	9	1	ADR36040	Human nicking agen
	36	8.4	42.0	10	1	AAV05484	BsmAI restriction
c	37	8.4	42.0	10	1	AAZ78224	Human dendritic ce
c	38	8.4	42.0	10	1	AAZ82947	Metastatic breast
	39	8.4	42.0	10	1	AAZ83008	Metastatic breast
c	40	8.4	42.0	10	1	AAZ86119	Metastatic breast
c	41	8.4	42.0	10	1	AAS04430	Human DAXX DNA pri
c	42	8.4	42.0	10	1	AAF38748	Yeast NORF gene SA
	43	8.4	42.0	10	1	AAF42997	Yeast NORF gene SA
c	44	8.4	42.0	10	1	AAF38731	Yeast NORF gene SA
c	45	8.4	42.0	10	1	AAF33728	Yeast NORF gene SA
	46	8.4	42.0	10	1	AAF34179	Yeast NORF gene SA
c	47	8.4	42.0	10	1	AAF39592	Yeast NORF gene SA
	48	8.4	42.0	10	1	AAF38171	Yeast NORF gene SA
c	49	8.4	42.0	10	1	AAF39425	Yeast NORF gene SA
c	50	8.4	42.0	10	1	AAF41789	Yeast NORF gene SA
c	51	8.4	42.0	10	1	AAF34632	Yeast NORF gene SA
c	52	8.4	42.0	10	1	AAS98827	Colony stimulating
c	53	8.4	42.0	10	1	ACC41713	Zinc finger protei
	54	8.4	42.0	10	1	ADH69419	Exon 4/5 junction
c	55	8.4	42.0	10	1	ADP47134	Human phospholipas
c	56	8.4	42.0	10	1	ADZ67944	NTRK1 gene polymor
c	57	8.4	42.0	10	1	AEA62012	NTRK1 gene polymor
	58	8	40.0	8	1	AAT09601	3'-primer used for
c	59	8	40.0	8	1	AAT09436	5'-primer used for
c	60	8	40.0	8	1	AAA80951	A. thaliana primer
c	61	8	40.0	8	1	AAA80762	A. thaliana primer
c	62	8	40.0	8	1	AAA81188	A. thaliana primer
	63	8	40.0	10	1	AAQ88288	5'-target sequence
c	64	8	40.0	10	1	AAQ88294	Primer sequence 8
	65	8	40.0	10	1	AAV50258	Yeast tag for addi
c	66	8	40.0	10	1	AAZ08343	Nilaparvata lugens
	67	8	40.0	10	1	AAZ81566	Metastatic breast
c	68	8	40.0	10	1	AAZ86307	Metastatic breast
c	69	8	40.0	10	1	AAZ83592	Metastatic breast
	70	8	40.0	10	1	AAZ85035	Metastatic breast
	71	8	40.0	10	1	AAZ81791	Metastatic breast
c	72	8	40.0	10	1	AAZ83176	Metastatic breast
c	73	8	40.0	10	1	AAZ80874	Metastatic breast
	74	8	40.0	10	1	AAC74005	Human dendritic ce
	75	8	40.0	10	1	AAA56168	Human monocyte gen
c	76	8	40.0	10	1	AAA70756	PCR primer #2 for
	77	8	40.0	10	1	AAH63895	Human ubiquitously
	78	8	40.0	10	1	AAH63530	Human ubiquitously
c	79	8	40.0	10	1	AAH41695	Anti-PEP gene cons
c	80	8	40.0	10	1	AAF69645	Human IL4Ralpha ge
	81	8	40.0	10	1	AAF38187	Yeast NORF gene SA
	82	8	40.0	10	1	AAF39032	Yeast NORF gene SA
	83	8	40.0	10	1	AAF36782	Yeast NORF gene SA
	84	8	40.0	10	1	AAF43826	Yeast NORF gene SA
c	85	8	40.0	10	1	AAF41988	Yeast NORF gene SA
	86	8	40.0	10	1	AAF33475	Yeast NORF gene SA
	87	8	40.0	10	1	AAF41634	Yeast NORF gene SA
	88	8	40.0	10	1	AAS95346	Human Histamine H2
	89	8	40.0	10	1	ABL60204	Human MUC1 PCR pri
	90	8	40.0	10	1	AAD25917	Human MC4R gene po
c	91	8	40.0	10	1	AAS95397	Human ICAM2 gene a
c	92	8	40.0	10	1	ABV78460	Human Th1 cell pre
	93	8	40.0	10	1	ABV78336	Human ribosomal pr
	94	8	40.0	10	1	ABK23747	Transcript tag DNA
	95	8	40.0	10	1	ABK23710	Transcript tag DNA
	96	8	40.0	10	1	AAS97350	Human CRYBB1 gene
	97	8	40.0	10	1	ACA94446	DNA tag from human
c	98	8	40.0	10	1	ABT14242	Nucleic acid PCR a
	99	8	40.0	10	1	ADA00650	Oligonucleotide mi
c	100	8	40.0	10	1	ADL96158	CD15+ myeloid cell
	101	8	40.0	10	1	ADI53195	Human CD3E primer
c	102	8	40.0	10	1	ADK69774	Type 2 helper T (T
	103	8	40.0	10	1	ADS77586	Breast cancer dete
	104	8	40.0	10	1	ADS76686	Breast cancer dete
	105	8	40.0	10	1	ADS77754	Breast cancer dete
	106	8	40.0	10	1	ADZ85566	Human BACE455 cDNA

107	5.2	26.0	10	1	AAZ86307	Metastatic breast
c 108	5.2	26.0	10	1	AAZ81791	Metastatic breast
109	4.8	24.0	10	1	AAF39425	Yeast NORF gene SA
110	4.8	24.0	11	1	ADQ32655	Human facial skin-
c 111	4.4	22.0	10	1	AAF42075	Yeast NORF gene SA
c 112	4.4	22.0	10	1	AAZ81566	Metastatic breast
c 113	4.2	21.0	10	1	AAQ88288	5'-target sequence
114	4.2	21.0	10	1	AAQ88294	Primer sequence 8
115	4.2	21.0	10	1	AAZ08343	Nilaparvata lugens
116	4.2	21.0	10	1	AAA70756	PCR primer #2 for
117	4.2	21.0	10	1	AAH41695	Anti-PEP gene cons
118	4.2	21.0	10	1	ABT14242	Nucleic acid PCR a
119	4.2	21.0	10	1	ADK69774	Type 2 helper T (T
c 120	4.2	21.0	10	1	ADZ85566	Human BACE455 cDNA
121	4	20.0	9	1	ADR36038	Human nicking agen
122	4	20.0	9	1	ADR36039	Human nicking agen
123	4	20.0	9	1	ADR36041	Human nicking agen
124	4	20.0	9	1	ADR36040	Human nicking agen
c 125	4	20.0	11	1	ABV69205	Human skin EST 699
126	3.6	18.0	10	1	AAS98827	Colony stimulating
c 127	3.6	18.0	11	1	ABV66235	Human skin EST 402
c 128	3.6	18.0	20	1	ADP69107	Human mitoNEET-spe
c 129	3.6	18.0	20	1	ADP69109	Human mitoNEET-spe
c 130	3.6	18.0	20	1	ADP69110	Human mitoNEET-spe
c 131	3.6	18.0	20	1	ADP69108	Human mitoNEET-spe
c 132	3.6	18.0	20	1	ADP69116	Human mitoNEET-spe
c 133	3.6	18.0	20	1	ADP69124	Human mitoNEET-spe
c 134	3.6	18.0	20	1	ADP69130	Human mitoNEET-spe
c 135	3.4	17.0	10	1	AAZ81653	Metastatic breast
136	3.4	17.0	10	1	ADU19570	Hypoxia-related tu
137	3.4	17.0	10	1	AAZ82947	Metastatic breast
c 138	3.4	17.0	10	1	AAZ83008	Metastatic breast
139	3.4	17.0	10	1	AAZ86119	Metastatic breast
c 140	3.4	17.0	10	1	AAF34179	Yeast NORF gene SA
141	3.4	17.0	10	1	AAF39592	Yeast NORF gene SA
c 142	3.4	17.0	10	1	AAF38171	Yeast NORF gene SA
143	3.4	17.0	10	1	ACC41713	Zinc finger protei
144	3.4	17.0	10	1	ADZ67944	NTRK1 gene polymor
145	3.4	17.0	10	1	AEA62012	NTRK1 gene polymor
146	3.4	17.0	10	1	AAZ83176	Metastatic breast
c 147	3.4	17.0	10	1	AAH63895	Human ubiquitously
148	3.4	17.0	10	1	AAF41988	Yeast NORF gene SA
c 149	3.4	17.0	10	1	AAD25917	Human MC4R gene po
150	3.4	17.0	10	1	ABV78460	Human Th1 cell pre
c 151	3.4	17.0	10	1	ABK23710	Transcript tag DNA
c 152	3.4	17.0	10	1	ADA00650	Oligonucleotide mi
153	3.4	17.0	11	1	ABV64201	Human skin EST 198
154	3.4	17.0	11	1	ABV71622	Human skin EST 940
155	3.4	17.0	11	1	ABQ87397	Human skin stress/
156	3.4	17.0	11	1	ABV65400	Human skin EST 318
157	3.4	17.0	17	1	ABN09352	Human GDMLP-1 17-m
158	3.4	17.0	17	1	ABN09353	Human GDMLP-1 17-m
159	3.4	17.0	17	1	ABN09354	Human GDMLP-1 17-m
160	3.4	17.0	17	1	ACN72443	Human GDMLP-1 prob
161	3.4	17.0	17	1	ACN72442	Human GDMLP-1 prob
162	3.4	17.0	17	1	ACN72444	Human GDMLP-1 prob
c 163	3.4	17.0	20	1	ADP69113	Human mitoNEET-spe
c 164	3.4	17.0	20	1	ADP69111	Human mitoNEET-spe
c 165	3.2	16.0	8	1	AAT09601	3'-primer used for
166	3.2	16.0	8	1	AAT09436	5'-primer used for
167	3.2	16.0	10	1	AAZ78224	Human dendritic ce
168	3.2	16.0	10	1	AAZ80874	Metastatic breast
c 169	3.2	16.0	10	1	AAS95346	Human Histamine H2
170	3.2	16.0	11	1	ABV70379	Human skin EST 816
171	3.2	16.0	11	1	ABV62958	Human skin EST 744
c 172	3	15.0	10	1	AAV05484	BsmAI restriction
173	3	15.0	10	1	AAF41789	Yeast NORF gene SA
174	3	15.0	10	1	AAF69645	Human IL4Ralpha ge
175	2.8	14.0	8	1	AAA81188	A. thaliana primer
c 176	2.8	14.0	10	1	ADH69419	Exon 4/5 junction
c 177	2.8	14.0	10	1	AAV50258	Yeast tag for addi
178	2.8	14.0	10	1	AAZ83592	Metastatic breast
c 179	2.8	14.0	10	1	AAZ85035	Metastatic breast
c 180	2.8	14.0	10	1	AAC74005	Human dendritic ce
c 181	2.8	14.0	10	1	AAA56168	Human monocyte gen
c 182	2.8	14.0	10	1	AAH63530	Human ubiquitously
c 183	2.8	14.0	10	1	AAF38187	Yeast NORF gene SA
c 184	2.8	14.0	10	1	AAF39032	Yeast NORF gene SA
c 185	2.8	14.0	10	1	AAF33475	Yeast NORF gene SA
c 186	2.8	14.0	10	1	ABL60204	Human MUC1 PCR pri
c 187	2.8	14.0	10	1	ABV78336	Human ribosomal pr
c 188	2.8	14.0	10	1	ABK23747	Transcript tag DNA
c 189	2.8	14.0	10	1	ACA94446	DNA tag from human
190	2.8	14.0	10	1	ADL96158	CD15+ myeloid cell
c 191	2.8	14.0	10	1	ADI53195	Human CD3E primer
c 192	2.8	14.0	10	1	ADS77586	Breast cancer dete
c 193	2.8	14.0	10	1	ADS76686	Breast cancer dete
c 194	2.8	14.0	10	1	ADS77754	Breast cancer dete
195	2.4	12.0	8	1	AAA80951	A. thaliana primer
196	2.4	12.0	8	1	AAA80762	A. thaliana primer
197	2.4	12.0	10	1	AAS04430	Human DAXX DNA pri
c 198	2.4	12.0	10	1	AAF42997	Yeast NORF gene SA
199	2.4	12.0	10	1	ADP47134	Human phospholipas
c 200	2.4	12.0	10	1	AAF43826	Yeast NORF gene SA
c 201	2.4	12.0	10	1	AAF41634	Yeast NORF gene SA
202	2.4	12.0	10	1	AAS95397	Human ICAM2 gene a
c 203	2.4	12.0	10	1	AAS97350	Human CRYBB1 gene
204	2.4	12.0	13	1	ABF03676	Oligonucleotide SE
c 205	2.4	12.0	13	1	ABF03677	Oligonucleotide SE
206	2.2	11.0	11	1	ADQ33489	Human facial skin-
207	2	10.0	10	1	AAF38748	Yeast NORF gene SA
208	2	10.0	10	1	AAF38731	Yeast NORF gene SA
209	2	10.0	10	1	AAF33728	Yeast NORF gene SA
210	2	10.0	10	1	AAF34632	Yeast NORF gene SA
c 211	2	10.0	10	1	AAF36782	Yeast NORF gene SA
212	2	10.0	11	1	ADG64354	DNA polymerase 3'-

ALIGNMENTS

RESULT 1
ADP69107
ID ADP69107 standard; DNA; 20 BP.
XX
AC ADP69107;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human mitoNEET-specific antisense oligonucleotide #1.
XX
KW human; antisense oligonucleotide; mitochondrial membrane;
KW insulin sensitising antidiabetic thiazolodinediones; mitoNEET; diabetes;
KW immunological disorder; cardiovascular disorder; including hypertension;
KW neurological disorders; ischaemia; reperfusion; ss;
KW 2'-methoxyethyl gapmer; 2'-MOE gapmer; phosphorothioate backbone.
XX
OS Homo sapiens.
XX
PN WO2004053060-A2.
XX
PD 24-JUN-2004.
XX
PF 25-NOV-2003; 2003WO-US037621.
XX
PR 06-DEC-2002; 2002US-0431529P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Colca JR;
XX
DR WPI; 2004-468836/44.
XX
PT New antisense oligonucleotides encoding mitoNEET, useful for modulating
PT mitoNEET expression or for treating diseases associated with mitoNEET,
PT e.g. diabetes, immunological disorders or cardiovascular disorders.

```
XX
PS   Claim 4; SEQ ID NO 1; 226pp; English.
XX
CC   The invention comprises antisense oligonucleotides that are targeted to
CC   the nucleic acids encoding a family of human proteins from mitochondrial
CC   membranes, which bind insulin sensitising, antidiabetic
CC   thiazolodinediones (referred to as: mitoNEET). The antisense
CC   oligonucleotides of the invention are useful for modulating mitoNEET
CC   expression and for treating diseases or conditions associated with
CC   mitoNEET, such as: diabetes, immunological disorders, cardiovascular
CC   disorders including hypertension, neurological disorders, and
CC   ischaemia/reperfusion injuries. The present DNA sequence represents a
CC   mitoNEET-specific antisense oligonucleotide of the invention. NOTE: The
CC   present sequence is a 2'-methoxyethyl (2'-MOE) gapmer with a
CC   phosphorothioate backbone.
XX
SQ   Sequence 20 BP; 1 A; 6 C; 3 G; 10 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTGTCTCCAGTCTCTTCGTT 20
              ||||||||||||||||||||
Db          1 TTGTCTCCAGTCTCTTCGTT 20


RESULT 2
ADP69109
ID   ADP69109 standard; DNA; 20 BP.
XX
AC   ADP69109;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human mitoNEET-specific antisense oligonucleotide #3.
XX
KW   human; antisense oligonucleotide; mitochondrial membrane;
KW   insulin sensitising antidiabetic thiazolodinediones; mitoNEET; diabetes;
KW   immunological disorder; cardiovascular disorder; including hypertension;
KW   neurological disorders; ischaemia; reperfusion; ss;
KW   2'-methoxyethyl gapmer; 2'-MOE gapmer; phosphorothioate backbone.
XX
OS   Homo sapiens.
XX
PN   WO2004053060-A2.
XX
PD   24-JUN-2004.
XX
PF   25-NOV-2003; 2003WO-US037621.
XX
PR   06-DEC-2002; 2002US-0431529P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Colca JR;
XX
DR   WPI; 2004-468836/44.
XX
PT   New antisense oligonucleotides encoding mitoNEET, useful for modulating
PT   mitoNEET expression or for treating diseases associated with mitoNEET,
PT   e.g. diabetes, immunological disorders or cardiovascular disorders.
XX
PS   Claim 4; SEQ ID NO 3; 226pp; English.
XX
CC   The invention comprises antisense oligonucleotides that are targeted to
CC   the nucleic acids encoding a family of human proteins from mitochondrial
CC   membranes, which bind insulin sensitising, antidiabetic
CC   thiazolodinediones (referred to as: mitoNEET). The antisense
CC   oligonucleotides of the invention are useful for modulating mitoNEET
CC   expression and for treating diseases or conditions associated with
CC   mitoNEET, such as: diabetes, immunological disorders, cardiovascular
CC   disorders including hypertension, neurological disorders, and
CC   ischaemia/reperfusion injuries. The present DNA sequence represents a
CC   mitoNEET-specific antisense oligonucleotide of the invention. NOTE: The
CC   present sequence is a 2'-methoxyethyl (2'-MOE) gapmer with a
CC   phosphorothioate backbone.
XX
SQ   Sequence 20 BP; 2 A; 6 C; 3 G; 9 T; 0 U; 0 Other;

  Query Match             95.0%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.3;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TGTCTCCAGTCTCTTCGTT 20
              |||||||||||||||||||
Db          1 TGTCTCCAGTCTCTTCGTT 19


RESULT 3
ADP69110
ID   ADP69110 standard; DNA; 20 BP.
XX
AC   ADP69110;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human mitoNEET-specific antisense oligonucleotide #4.
XX
KW   human; antisense oligonucleotide; mitochondrial membrane;
KW   insulin sensitising antidiabetic thiazolodinediones; mitoNEET; diabetes;
KW   immunological disorder; cardiovascular disorder; including hypertension;
KW   neurological disorders; ischaemia; reperfusion; ss;
KW   2'-methoxyethyl gapmer; 2'-MOE gapmer; phosphorothioate backbone.
XX
OS   Homo sapiens.
XX
PN   WO2004053060-A2.
XX
PD   24-JUN-2004.
XX
PF   25-NOV-2003; 2003WO-US037621.
XX
PR   06-DEC-2002; 2002US-0431529P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Colca JR;
XX
DR   WPI; 2004-468836/44.
XX
PT   New antisense oligonucleotides encoding mitoNEET, useful for modulating
PT   mitoNEET expression or for treating diseases associated with mitoNEET,
PT   e.g. diabetes, immunological disorders or cardiovascular disorders.
XX
PS   Claim 4; SEQ ID NO 4; 226pp; English.
XX
CC   The invention comprises antisense oligonucleotides that are targeted to
CC   the nucleic acids encoding a family of human proteins from mitochondrial
CC   membranes, which bind insulin sensitising, antidiabetic
CC   thiazolodinediones (referred to as: mitoNEET). The antisense
CC   oligonucleotides of the invention are useful for modulating mitoNEET
CC   expression and for treating diseases or conditions associated with
CC   mitoNEET, such as: diabetes, immunological disorders, cardiovascular
CC   disorders including hypertension, neurological disorders, and
CC   ischaemia/reperfusion injuries. The present DNA sequence represents a
CC   mitoNEET-specific antisense oligonucleotide of the invention. NOTE: The
CC   present sequence is a 2'-methoxyethyl (2'-MOE) gapmer with a
CC   phosphorothioate backbone.
XX
SQ   Sequence 20 BP; 2 A; 6 C; 3 G; 9 T; 0 U; 0 Other;

  Query Match             95.0%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.3;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 TTGTCTCCAGTCTCTTCGT 19
              ||||||||||||||||||
Db          2 TTGTCTCCAGTCTCTTCGT 20
```

```
RESULT 4
ADP69108
ID   ADP69108 standard; DNA; 20 BP.
XX
AC   ADP69108;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human mitoNEET-specific antisense oligonucleotide #2.
XX
KW   human; antisense oligonucleotide; mitochondrial membrane;
KW   insulin sensitising antidiabetic thiazolodinediones; mitoNEET; diabetes;
KW   immunological disorder; cardiovascular disorder; including hypertension;
KW   neurological disorders; ischaemia; reperfusion; ss;
KW   2'-methoxyethyl gapmer; 2'-MOE gapmer; phosphorothioate backbone.
XX
OS   Homo sapiens.
XX
PN   WO2004053060-A2.
XX
PD   24-JUN-2004.
XX
PF   25-NOV-2003; 2003WO-US037621.
XX
PR   06-DEC-2002; 2002US-0431529P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Colca JR;
XX
DR   WPI; 2004-468836/44.
XX
PT   New antisense oligonucleotides encoding mitoNEET, useful for modulating
PT   mitoNEET expression or for treating diseases associated with mitoNEET,
PT   e.g. diabetes, immunological disorders or cardiovascular disorders.
XX
PS   Claim 4; SEQ ID NO 2; 226pp; English.
XX
CC   The invention comprises antisense oligonucleotides that are targeted to
CC   the nucleic acids encoding a family of human proteins from mitochondrial
CC   membranes, which bind insulin sensitising, antidiabetic
CC   thiazolodinediones (referred to as: mitoNEET). The antisense
CC   oligonucleotides of the invention are useful for modulating mitoNEET
CC   expression and for treating diseases or conditions associated with
CC   mitoNEET, such as: diabetes, immunological disorders, cardiovascular
CC   disorders including hypertension, neurological disorders, and
CC   ischaemia/reperfusion injuries. The present DNA sequence represents a
CC   mitoNEET-specific antisense oligonucleotide of the invention. NOTE: The
CC   present sequence is a 2'-methoxyethyl (2'-MOE) gapmer with a
CC   phosphorothioate backbone.
XX
SQ   Sequence 20 BP; 2 A; 6 C; 3 G; 9 T; 0 U; 0 Other;

  Query Match             90.0%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.3;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAGTCTCTTCGTT 20
              ||||||||||||||||||
Db          1 GTCTCCAGTCTCTTCGTT 18
```

```
RESULT 5
ADP69116
ID   ADP69116 standard; DNA; 20 BP.
XX
AC   ADP69116;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human mitoNEET-specific antisense oligonucleotide #10.
XX
KW   human; antisense oligonucleotide; mitochondrial membrane;
KW   insulin sensitising antidiabetic thiazolodinediones; mitoNEET; diabetes;
KW   immunological disorder; cardiovascular disorder; including hypertension;
KW   neurological disorders; ischaemia; reperfusion; ss;
KW   2'-methoxyethyl gapmer; 2'-MOE gapmer; phosphorothioate backbone.
XX
OS   Homo sapiens.
XX
PN   WO2004053060-A2.
XX
PD   24-JUN-2004.
XX
PF   25-NOV-2003; 2003WO-US037621.
XX
PR   06-DEC-2002; 2002US-0431529P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Colca JR;
XX
DR   WPI; 2004-468836/44.
XX
PT   New antisense oligonucleotides encoding mitoNEET, useful for modulating
PT   mitoNEET expression or for treating diseases associated with mitoNEET,
PT   e.g. diabetes, immunological disorders or cardiovascular disorders.
XX
PS   Claim 4; SEQ ID NO 10; 226pp; English.
XX
CC   The invention comprises antisense oligonucleotides that are targeted to
CC   the nucleic acids encoding a family of human proteins from mitochondrial
CC   membranes, which bind insulin sensitising, antidiabetic
CC   thiazolodinediones (referred to as: mitoNEET). The antisense
CC   oligonucleotides of the invention are useful for modulating mitoNEET
CC   expression and for treating diseases or conditions associated with
CC   mitoNEET, such as: diabetes, immunological disorders, cardiovascular
CC   disorders including hypertension, neurological disorders, and
CC   ischaemia/reperfusion injuries. The present DNA sequence represents a
CC   mitoNEET-specific antisense oligonucleotide of the invention. NOTE: The
CC   present sequence is a 2'-methoxyethyl (2'-MOE) gapmer with a
CC   phosphorothioate backbone.
XX
SQ   Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;

  Query Match             90.0%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.3;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTGTCTCCAGTCTCTTCG 18
              ||||||||||||||||||
Db          3 TTGTCTCCAGTCTCTTCG 20
```

```
RESULT 6
ADP69124
ID   ADP69124 standard; DNA; 20 BP.
XX
AC   ADP69124;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human mitoNEET-specific antisense oligonucleotide #18.
XX
KW   human; antisense oligonucleotide; mitochondrial membrane;
KW   insulin sensitising antidiabetic thiazolodinediones; mitoNEET; diabetes;
KW   immunological disorder; cardiovascular disorder; including hypertension;
KW   neurological disorders; ischaemia; reperfusion; ss;
KW   2'-methoxyethyl gapmer; 2'-MOE gapmer; phosphorothioate backbone.
XX
OS   Homo sapiens.
```

XX
PN WO2004053060-A2.
XX
PD 24-JUN-2004.
XX
PF 25-NOV-2003; 2003WO-US037621.
XX
PR 06-DEC-2002; 2002US-0431529P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Colca JR;
XX
DR WPI; 2004-468836/44.
XX
PT New antisense oligonucleotides encoding mitoNEET, useful for modulating
PT mitoNEET expression or for treating diseases associated with mitoNEET,
PT e.g. diabetes, immunological disorders or cardiovascular disorders.
XX
PS Claim 4; SEQ ID NO 18; 226pp; English.
XX
CC The invention comprises antisense oligonucleotides that are targeted to
CC the nucleic acids encoding a family of human proteins from mitochondrial
CC membranes, which bind insulin sensitising, antidiabetic
CC thiazolodinediones (referred to as: mitoNEET). The antisense
CC oligonucleotides of the invention are useful for modulating mitoNEET
CC expression and for treating diseases or conditions associated with
CC mitoNEET, such as: diabetes, immunological disorders, cardiovascular
CC disorders including hypertension, neurological disorders, and
CC ischaemia/reperfusion injuries. The present DNA sequence represents a
CC mitoNEET-specific antisense oligonucleotide of the invention. NOTE: The
CC present sequence is a 2'-methoxyethyl (2'-MOE) gapmer with a
CC phosphorothioate backbone.
XX
SQ Sequence 20 BP; 3 A; 7 C; 2 G; 8 T; 0 U; 0 Other;

```
  Query Match             85.0%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.7;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTGTCTCCAGTCTCTTC 17
              |||||||||||||||||
Db          4 TTGTCTCCAGTCTCTTC 20
```

RESULT 7
ADP69113
ID ADP69113 standard; DNA; 20 BP.
XX
AC ADP69113;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human mitoNEET-specific antisense oligonucleotide #7.
XX
KW human; antisense oligonucleotide; mitochondrial membrane;
KW insulin sensitising antidiabetic thiazolodinediones; mitoNEET; diabetes;
KW immunological disorder; cardiovascular disorder; including hypertension;
KW neurological disorders; ischaemia; reperfusion; ss;
KW 2'-methoxyethyl gapmer; 2'-MOE gapmer; phosphorothioate backbone.
XX
OS Homo sapiens.
XX
PN WO2004053060-A2.
XX
PD 24-JUN-2004.
XX
PF 25-NOV-2003; 2003WO-US037621.
XX
PR 06-DEC-2002; 2002US-0431529P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Colca JR;
XX
DR WPI; 2004-468836/44.
XX
PT New antisense oligonucleotides encoding mitoNEET, useful for modulating
PT mitoNEET expression or for treating diseases associated with mitoNEET,
PT e.g. diabetes, immunological disorders or cardiovascular disorders.
XX
PS Claim 4; SEQ ID NO 7; 226pp; English.
XX
CC The invention comprises antisense oligonucleotides that are targeted to
CC the nucleic acids encoding a family of human proteins from mitochondrial
CC membranes, which bind insulin sensitising, antidiabetic
CC thiazolodinediones (referred to as: mitoNEET). The antisense
CC oligonucleotides of the invention are useful for modulating mitoNEET
CC expression and for treating diseases or conditions associated with
CC mitoNEET, such as: diabetes, immunological disorders, cardiovascular
CC disorders including hypertension, neurological disorders, and
CC ischaemia/reperfusion injuries. The present DNA sequence represents a
CC mitoNEET-specific antisense oligonucleotide of the invention. NOTE: The
CC present sequence is a 2'-methoxyethyl (2'-MOE) gapmer with a
CC phosphorothioate backbone.
XX
SQ Sequence 20 BP; 2 A; 6 C; 3 G; 9 T; 0 U; 0 Other;

```
  Query Match             85.0%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.7;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TCTCCAGTCTCTTCGTT 20
              |||||||||||||||||
Db          1 TCTCCAGTCTCTTCGTT 17
```

RESULT 8
ADP69111
ID ADP69111 standard; DNA; 20 BP.
XX
AC ADP69111;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human mitoNEET-specific antisense oligonucleotide #5.
XX
KW human; antisense oligonucleotide; mitochondrial membrane;
KW insulin sensitising antidiabetic thiazolodinediones; mitoNEET; diabetes;
KW immunological disorder; cardiovascular disorder; including hypertension;
KW neurological disorders; ischaemia; reperfusion; ss;
KW 2'-methoxyethyl gapmer; 2'-MOE gapmer; phosphorothioate backbone.
XX
OS Homo sapiens.
XX
PN WO2004053060-A2.
XX
PD 24-JUN-2004.
XX
PF 25-NOV-2003; 2003WO-US037621.
XX
PR 06-DEC-2002; 2002US-0431529P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Colca JR;
XX
DR WPI; 2004-468836/44.
XX
PT New antisense oligonucleotides encoding mitoNEET, useful for modulating
PT mitoNEET expression or for treating diseases associated with mitoNEET,
PT e.g. diabetes, immunological disorders or cardiovascular disorders.
XX
PS Claim 4; SEQ ID NO 5; 226pp; English.
XX
CC The invention comprises antisense oligonucleotides that are targeted to

```
CC   the nucleic acids encoding a family of human proteins from mitochondrial
CC   membranes, which bind insulin sensitising, antidiabetic
CC   thiazolodinediones (referred to as: mitoNEET). The antisense
CC   oligonucleotides of the invention are useful for modulating mitoNEET
CC   expression and for treating diseases or conditions associated with
CC   mitoNEET, such as: diabetes, immunological disorders, cardiovascular
CC   disorders including hypertension, neurological disorders, and
CC   ischaemia/reperfusion injuries. The present DNA sequence represents a
CC   mitoNEET-specific antisense oligonucleotide of the invention. NOTE: The
CC   present sequence is a 2'-methoxyethyl (2'-MOE) gapmer with a
CC   phosphorothioate backbone.
XX
SQ   Sequence 20 BP; 2 A; 6 C; 3 G; 9 T; 0 U; 0 Other;

  Query Match             80.0%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.8;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CTCCAGTCTCTTCGTT 20
              ||||||||||||||||
Db          1 CTCCAGTCTCTTCGTT 16


RESULT 9
ADP69130
ID   ADP69130 standard; DNA; 20 BP.
XX
AC   ADP69130;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human mitoNEET-specific antisense oligonucleotide #24.
XX
KW   human; antisense oligonucleotide; mitochondrial membrane;
KW   insulin sensitising antidiabetic thiazolodinediones; mitoNEET; diabetes;
KW   immunological disorder; cardiovascular disorder; including hypertension;
KW   neurological disorders; ischaemia; reperfusion; ss;
KW   2'-methoxyethyl gapmer; 2'-MOE gapmer; phosphorothioate backbone.
XX
OS   Homo sapiens.
XX
PN   WO2004053060-A2.
XX
PD   24-JUN-2004.
XX
PF   25-NOV-2003; 2003WO-US037621.
XX
PR   06-DEC-2002; 2002US-0431529P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Colca JR;
XX
DR   WPI; 2004-468836/44.
XX
PT   New antisense oligonucleotides encoding mitoNEET, useful for modulating
PT   mitoNEET expression or for treating diseases associated with mitoNEET,
PT   e.g. diabetes, immunological disorders or cardiovascular disorders.
XX
PS   Claim 4; SEQ ID NO 24; 226pp; English.
XX
CC   The invention comprises antisense oligonucleotides that are targeted to
CC   the nucleic acids encoding a family of human proteins from mitochondrial
CC   membranes, which bind insulin sensitising, antidiabetic
CC   thiazolodinediones (referred to as: mitoNEET). The antisense
CC   oligonucleotides of the invention are useful for modulating mitoNEET
CC   expression and for treating diseases or conditions associated with
CC   mitoNEET, such as: diabetes, immunological disorders, cardiovascular
CC   disorders including hypertension, neurological disorders, and
CC   ischaemia/reperfusion injuries. The present DNA sequence represents a
CC   mitoNEET-specific antisense oligonucleotide of the invention. NOTE: The
CC   present sequence is a 2'-methoxyethyl (2'-MOE) gapmer with a
CC   phosphorothioate backbone.
XX
SQ   Sequence 20 BP; 3 A; 7 C; 2 G; 8 T; 0 U; 0 Other;

  Query Match             80.0%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 6.8;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTGTCTCCAGTCTCTT 16
              ||||||||||||||||
Db          5 TTGTCTCCAGTCTCTT 20


RESULT 10
ABN09352/c
ID   ABN09352 standard; DNA; 17 BP.
XX
AC   ABN09352;
XX
DT   29-MAY-2002  (first entry)
XX
DE   Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9344.
XX
KW   Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW   muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW   skeletal muscle disorder; amplicon; screening; ss.
XX
OS   Homo sapiens.
XX
PN   WO200192524-A2.
XX
PD   06-DEC-2001.
XX
PF   25-MAY-2001; 2001WO-US016981.
XX
PR   26-MAY-2000; 2000US-0207456P.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
PR   30-JAN-2001; 2001WO-US000661.
PR   30-JAN-2001; 2001WO-US000662.
PR   30-JAN-2001; 2001WO-US000663.
PR   30-JAN-2001; 2001WO-US000664.
PR   30-JAN-2001; 2001WO-US000665.
PR   30-JAN-2001; 2001WO-US000666.
PR   30-JAN-2001; 2001WO-US000667.
PR   30-JAN-2001; 2001WO-US000668.
PR   30-JAN-2001; 2001WO-US000669.
PR   30-JAN-2001; 2001WO-US000670.
PR   05-FEB-2001; 2001US-0266860P.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Gu Y,  Ji Y,  Penn SG,  Hanzel DK,  Rank DR,  Chen W,  Shannon ME;
XX
DR   WPI; 2002-179446/23.
XX
PT   New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT   or as specific biomolecule capture probes for surface-enhanced laser
PT   desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
PS   Disclosure; SEQ ID NO 9344; 214pp; English.
XX
CC   The present invention describes a human genome-derived myosin-like
CC   protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC   1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC   nucleic acids can be used as probes to detect, characterise and quantify
CC   hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC   provide initial substrates for the recombinant engineering of hGDMLP-1
CC   protein variants having desired phenotypic improvements, and for
CC   expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC   used as immunogens to raise antibodies that specifically recognise hGDMLP
CC   -1 proteins, as standards in assays used to determine the concentration
CC   and/or amount specifically of hGDMLP proteins, as specific biomolecule
```

```
CC   capture probes for surface-enhanced laser desorption ionisation, as
CC   therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC   production, and in vaccines or for replacement therapy. The
CC   polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC   disorder associated with the expression of hGDMLP-1, in particular heart
CC   and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC   The present sequence represents an oligomer used in the screening of the
CC   hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequence
XX
SQ   Sequence 17 BP; 6 A; 2 C; 8 G; 1 T; 0 U; 0 Other;

  Query Match            69.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity  88.2%;  Pred. No. 12;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 TCTCCAGTCTCTTCGTT 20
              || |||| |||||||||
Db         17 TCCCCAGCCTCTTCGTT 1


RESULT 11
ABN09353/c
ID   ABN09353 standard; DNA; 17 BP.
XX
AC   ABN09353;
XX
DT   29-MAY-2002  (first entry)
XX
DE   Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9345.
XX
KW   Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW   muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW   skeletal muscle disorder; amplicon; screening; ss.
XX
OS   Homo sapiens.
XX
PN   WO200192524-A2.
XX
PD   06-DEC-2001.
XX
PF   25-MAY-2001; 2001WO-US016981.
XX
PR   26-MAY-2000; 2000US-0207456P.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
PR   30-JAN-2001; 2001WO-US000661.
PR   30-JAN-2001; 2001WO-US000662.
PR   30-JAN-2001; 2001WO-US000663.
PR   30-JAN-2001; 2001WO-US000664.
PR   30-JAN-2001; 2001WO-US000665.
PR   30-JAN-2001; 2001WO-US000666.
PR   30-JAN-2001; 2001WO-US000667.
PR   30-JAN-2001; 2001WO-US000668.
PR   30-JAN-2001; 2001WO-US000669.
PR   30-JAN-2001; 2001WO-US000670.
PR   05-FEB-2001; 2001US-0266860P.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Gu Y,  Ji Y,  Penn SG,  Hanzel DK,  Rank DR,  Chen W,  Shannon ME;
XX
DR   WPI; 2002-179446/23.
XX
PT   New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT   or as specific biomolecule capture probes for surface-enhanced laser
PT   desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
PS   Disclosure; SEQ ID NO 9345; 214pp; English.
XX
CC   The present invention describes a human genome-derived myosin-like
CC   protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC   1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC   nucleic acids can be used as probes to detect, characterise and quantify
CC   hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC   provide initial substrates for the recombinant engineering of hGDMLP-1
CC   protein variants having desired phenotypic improvements, and for
CC   expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC   used as immunogens to raise antibodies that specifically recognise hGDMLP
CC   -1 proteins, as standards in assays used to determine the concentration
CC   and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC   capture probes for surface-enhanced laser desorption ionisation, as
CC   therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC   production, and in vaccines or for replacement therapy. The
CC   polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC   disorder associated with the expression of hGDMLP-1, in particular heart
CC   and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC   The present sequence represents an oligomer used in the screening of the
CC   hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequence
XX
SQ   Sequence 17 BP; 5 A; 3 C; 8 G; 1 T; 0 U; 0 Other;

  Query Match            69.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity  88.2%;  Pred. No. 12;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAGTCTCTTCGT 19
              ||| |||| |||||||||
Db         17 GTCCCCAGCCTCTTCGT 1


RESULT 12
ABN09354/c
ID   ABN09354 standard; DNA; 17 BP.
XX
AC   ABN09354;
XX
DT   29-MAY-2002  (first entry)
XX
DE   Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9346.
XX
KW   Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW   muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW   skeletal muscle disorder; amplicon; screening; ss.
XX
OS   Homo sapiens.
XX
PN   WO200192524-A2.
XX
PD   06-DEC-2001.
XX
PF   25-MAY-2001; 2001WO-US016981.
XX
PR   26-MAY-2000; 2000US-0207456P.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
PR   30-JAN-2001; 2001WO-US000661.
PR   30-JAN-2001; 2001WO-US000662.
PR   30-JAN-2001; 2001WO-US000663.
PR   30-JAN-2001; 2001WO-US000664.
PR   30-JAN-2001; 2001WO-US000665.
PR   30-JAN-2001; 2001WO-US000666.
PR   30-JAN-2001; 2001WO-US000667.
PR   30-JAN-2001; 2001WO-US000668.
PR   30-JAN-2001; 2001WO-US000669.
PR   30-JAN-2001; 2001WO-US000670.
PR   05-FEB-2001; 2001US-0266860P.
XX
PA   (AEOM-) AEOMICA INC.
```

```
XX
PI   Gu Y,  Ji Y,  Penn SG,  Hanzel DK,  Rank DR,  Chen W,  Shannon ME;
XX
DR   WPI; 2002-179446/23.
XX
PT   New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT   or as specific biomolecule capture probes for surface-enhanced laser
PT   desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
PS   Disclosure; SEQ ID NO 9346; 214pp; English.
XX
CC   The present invention describes a human genome-derived myosin-like
CC   protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC   1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC   nucleic acids can be used as probes to detect, characterise and quantify
CC   hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC   provide initial substrates for the recombinant engineering of hGDMLP-1
CC   protein variants having desired phenotypic improvements, and for
CC   expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC   used as immunogens to raise antibodies that specifically recognise hGDMLP
CC   -1 proteins, as standards in assays used to determine the concentration
CC   and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC   capture probes for surface-enhanced laser desorption ionisation, as
CC   therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC   production, and in vaccines or for replacement therapy. The
CC   polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC   disorder associated with the expression of hGDMLP-1, in particular heart
CC   and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC   The present sequence represents an oligomer used in the screening of the
CC   hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequence
XX
SQ   Sequence 17 BP; 5 A; 3 C; 8 G; 1 T; 0 U; 0 Other;

  Query Match             69.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 12;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TGTCTCCAGTCTCTTCG 18
              |||| |||| |||||||
Db         17 TGTCCCCAGCCTCTTCG 1


RESULT 13
ACN72443/c
ID   ACN72443 standard; DNA; 17 BP.
XX
AC   ACN72443;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Human GDMLP-1 probe SEQ ID NO:9345.
XX
KW   Human; ss; probe; myosin-like protein-1; hGDMLP-1;
KW   hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
KW   skeletal muscle function.
XX
OS   Homo sapiens.
XX
PN   US2004137589-A1.
XX
PD   15-JUL-2004.
XX
PF   26-NOV-2003; 2003US-00723361.
XX
PR   26-MAY-2000; 2000US-0207456P.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
PR   30-JAN-2001; 2001WO-US000661.
PR   30-JAN-2001; 2001WO-US000662.
PR   30-JAN-2001; 2001WO-US000663.
PR   30-JAN-2001; 2001WO-US000664.
PR   30-JAN-2001; 2001WO-US000665.
PR   30-JAN-2001; 2001WO-US000666.
PR   30-JAN-2001; 2001WO-US000667.
PR   30-JAN-2001; 2001WO-US000668.
PR   30-JAN-2001; 2001WO-US000669.
PR   30-JAN-2001; 2001WO-US000670.
PR   05-FEB-2001; 2001US-0266860P.
PR   25-MAY-2001; 2001US-00866108.
XX
PA   (GUYY/) GU Y.
PA   (JIYY/) JI Y.
PA   (PENN/) PENN S G.
PA   (HANZ/) HANZEL D K.
PA   (RANK/) RANK D.
PA   (CHEN/) CHEN W.
PA   (SHAN/) SHANNON M E.
XX
PI   Gu Y,  Ji Y,  Penn SG,  Hanzel DK,  Rank D,  Chen W,  Shannon ME;
XX
DR   WPI; 2004-533378/51.
XX
PT   Novel myosin-like protein-1, useful for treating or preventing disorder
PT   associated with decreased expression or activity of human genome-derived
PT   myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT   function.
XX
PS   Disclosure; SEQ ID NO 9345; 0pp; English.
XX
CC   The invention relates to a novel polypeptide (I) comprising a sequence
CC   (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully
CC   defined in the specification, a fragment of at least 8 amino acids of
CC   (S1), 95% deviation from (S1) which are conservative substitutions, and
CC   65% identity to (S1). A polypeptide of the invention acts as a agonist or
CC   antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A
CC   pharmaceutical composition of the invention is useful for treating or
CC   preventing a disorder associated with decreased expression or activity of
CC   hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
CC   The present sequence represents a 17-mer nucleotide, used in the
CC   invention for scanning the sequence represented in ACN63103
XX
SQ   Sequence 17 BP; 5 A; 3 C; 8 G; 1 T; 0 U; 0 Other;

  Query Match             69.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 12;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAGTCTCTTCGT 19
              ||| |||| ||||||||
Db         17 GTCCCCAGCCTCTTCGT 1


RESULT 14
ACN72442/c
ID   ACN72442 standard; DNA; 17 BP.
XX
AC   ACN72442;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Human GDMLP-1 probe SEQ ID NO:9344.
XX
KW   Human; ss; probe; myosin-like protein-1; hGDMLP-1;
KW   hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
KW   skeletal muscle function.
XX
OS   Homo sapiens.
XX
PN   US2004137589-A1.
XX
PD   15-JUL-2004.
XX
```

```
PF   26-NOV-2003; 2003US-00723361.
XX
PR   26-MAY-2000; 2000US-0207456P.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
PR   30-JAN-2001; 2001WO-US000661.
PR   30-JAN-2001; 2001WO-US000662.
PR   30-JAN-2001; 2001WO-US000663.
PR   30-JAN-2001; 2001WO-US000664.
PR   30-JAN-2001; 2001WO-US000665.
PR   30-JAN-2001; 2001WO-US000666.
PR   30-JAN-2001; 2001WO-US000667.
PR   30-JAN-2001; 2001WO-US000668.
PR   30-JAN-2001; 2001WO-US000669.
PR   30-JAN-2001; 2001WO-US000670.
PR   05-FEB-2001; 2001US-0266860P.
PR   25-MAY-2001; 2001US-00866108.
XX
PA   (GUYY/) GU Y.
PA   (JIYY/) JI Y.
PA   (PENN/) PENN S G.
PA   (HANZ/) HANZEL D K.
PA   (RANK/) RANK D.
PA   (CHEN/) CHEN W.
PA   (SHAN/) SHANNON M E.
XX
PI   Gu Y,  Ji Y,  Penn SG,  Hanzel DK,  Rank D,  Chen W,  Shannon ME;
XX
DR   WPI; 2004-533378/51.
XX
PT   Novel myosin-like protein-1, useful for treating or preventing disorder
PT   associated with decreased expression or activity of human genome-derived
PT   myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT   function.
XX
PS   Disclosure; SEQ ID NO 9344; 0pp; English.
XX
CC   The invention relates to a novel polypeptide (I) comprising a sequence
CC   (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully
CC   defined in the specification, a fragment of at least 8 amino acids of
CC   (S1), 95% deviation from (S1) which are conservative substitutions, and
CC   65% identity to (S1). A polypeptide of the invention acts as a agonist or
CC   antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A
CC   pharmaceutical composition of the invention is useful for treating or
CC   preventing a disorder associated with decreased expression or activity of
CC   hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
CC   The present sequence represents a 17-mer nucleotide, used in the
CC   invention for scanning the sequence represented in ACN63103
XX
SQ   Sequence 17 BP; 6 A; 2 C; 8 G; 1 T; 0 U; 0 Other;

  Query Match             69.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 12;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 TCTCCAGTCTCTTCGTT 20
              || |||| |||||||||
Db         17 TCCCCAGCCTCTTCGTT 1


RESULT 15
ACN72444/c
ID   ACN72444 standard; DNA; 17 BP.
XX
AC   ACN72444;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Human GDMLP-1 probe SEQ ID NO:9346.
XX
KW   Human; ss; probe; myosin-like protein-1; hGDMLP-1;
KW   hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
KW   skeletal muscle function.
XX
OS   Homo sapiens.
XX
PN   US2004137589-A1.
XX
PD   15-JUL-2004.
XX
PF   26-NOV-2003; 2003US-00723361.
XX
PR   26-MAY-2000; 2000US-0207456P.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
PR   30-JAN-2001; 2001WO-US000661.
PR   30-JAN-2001; 2001WO-US000662.
PR   30-JAN-2001; 2001WO-US000663.
PR   30-JAN-2001; 2001WO-US000664.
PR   30-JAN-2001; 2001WO-US000665.
PR   30-JAN-2001; 2001WO-US000666.
PR   30-JAN-2001; 2001WO-US000667.
PR   30-JAN-2001; 2001WO-US000668.
PR   30-JAN-2001; 2001WO-US000669.
PR   30-JAN-2001; 2001WO-US000670.
PR   05-FEB-2001; 2001US-0266860P.
PR   25-MAY-2001; 2001US-00866108.
XX
PA   (GUYY/) GU Y.
PA   (JIYY/) JI Y.
PA   (PENN/) PENN S G.
PA   (HANZ/) HANZEL D K.
PA   (RANK/) RANK D.
PA   (CHEN/) CHEN W.
PA   (SHAN/) SHANNON M E.
XX
PI   Gu Y,  Ji Y,  Penn SG,  Hanzel DK,  Rank D,  Chen W,  Shannon ME;
XX
DR   WPI; 2004-533378/51.
XX
PT   Novel myosin-like protein-1, useful for treating or preventing disorder
PT   associated with decreased expression or activity of human genome-derived
PT   myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT   function.
XX
PS   Disclosure; SEQ ID NO 9346; 0pp; English.
XX
CC   The invention relates to a novel polypeptide (I) comprising a sequence
CC   (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully
CC   defined in the specification, a fragment of at least 8 amino acids of
CC   (S1), 95% deviation from (S1) which are conservative substitutions, and
CC   65% identity to (S1). A polypeptide of the invention acts as a agonist or
CC   antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A
CC   pharmaceutical composition of the invention is useful for treating or
CC   preventing a disorder associated with decreased expression or activity of
CC   hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
CC   The present sequence represents a 17-mer nucleotide, used in the
CC   invention for scanning the sequence represented in ACN63103
XX
SQ   Sequence 17 BP; 5 A; 3 C; 8 G; 1 T; 0 U; 0 Other;

  Query Match             69.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 12;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TGTCTCCAGTCTCTTCG 18
              |||| |||| |||||||
Db         17 TGTCCCCAGCCTCTTCG 1


RESULT 16
ABF03676/c
ID   ABF03676 standard; DNA; 13 BP.
XX
```

```
AC   ABF03676;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 103673 for detecting SNP TSC0025934.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 103673; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 5 A; 1 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             52.0%;  Score 10.4;  DB 1;  Length 13;
  Best Local Similarity   91.7%;  Pred. No. 27;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCTCCAGTCTCT 15
              ||||| ||||||
Db         13 TCTCCCGTCTCT 2


RESULT 17
ABF03677
ID   ABF03677 standard; DNA; 13 BP.
XX
AC   ABF03677;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 103674 for detecting SNP TSC0025934.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 103674; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 1 A; 6 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             52.0%;  Score 10.4;  DB 1;  Length 13;
  Best Local Similarity   91.7%;  Pred. No. 27;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCTCCAGTCTCT 15
              ||||| ||||||
Db          1 TCTCCCGTCTCT 12


RESULT 18
ABV64201/c
ID   ABV64201 standard; cDNA; 11 BP.
XX
AC   ABV64201;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 1987.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
```

PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 80; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 3 A; 1 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 30;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 CCAGTCTCTTC 17
|||| ||||||
Db 11 CCAGCCTCTTC 1

RESULT 19
ABV71622/c
ID ABV71622 standard; cDNA; 11 BP.
XX
AC ABV71622;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 9408.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Claim 24; Page 303; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 3 A; 1 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 30;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 CCAGTCTCTTC 17
|||| ||||||
Db 11 CCAGCCTCTTC 1

RESULT 20
ADQ33489/c
ID ADQ33489 standard; DNA; 11 BP.
XX
AC ADQ33489;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human facial skin-associated DNA fragment SEQ ID NO 1579.
XX
KW facial skin; human; serial analysis of gene expression; SAGE;
KW homeostasis; biochip; cosmetic; pharmaceutical; ds.
XX
OS Homo sapiens.
XX
PN DE10260928-A1.
XX
PD 08-JUL-2004.
XX
PF 20-DEC-2002; 2002DE-01060928.
XX
PR 20-DEC-2002; 2002DE-01060928.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
PI Conradt M, Hofmann K;
XX
DR WPI; 2004-518855/50.
XX
PT In vitro identification of genes important for facial skin, useful for
PT assessing homeostasis and in screening for pharmaceutical or cosmetic
PT agents, based on differential expression analysis.
XX
PS Claim 5; SEQ ID NO 1579; 577pp; German.
XX
CC This invention describes a novel in vitro method for identifying genes
CC that are significant for facial skin in humans. The method comprises
CC recovering, from facial skin, a first mixture of genetically expressed
CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or
CC their fragments), recovering a second, similar mixture from some other
CC human tissue, preferably skin from a protected area, especially from the
CC breast and subjecting the mixtures to serial analysis of gene expression
CC (SAGE) to identify those genes for which expression is markedly different
CC between facial skin and the other tissue. The invention also describes an
CC in vitro method for determining homeostasis of human facial skin; a test
CC kit which comprises a solid support (flexible or rigid) on which are
CC immobilised probes that bind specifically to the factors of interest and
CC a biochip for determining homeostasis of human facial skin. The products
CC of the invention are also used in a method which determines activity of
CC cosmetic and pharmaceutical agents for use against disorders or
CC disturbances of the homeostasis of human skin and a screening method for
CC identifying cosmetic and pharmaceutical agents. The method allows
CC identification of as many as possible of the genes important for facial
CC skin and thus of a very wide range of potential therapeutic and cosmetic
CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to

```
CC   identify the facial skin-associated genes described in the invention.
XX
SQ   Sequence 11 BP; 5 A; 1 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 30;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 CCAGTCTCTTC 17
              ||||| |||||
Db         11 CCAGTTTCTTC 1


RESULT 21
ADQ32655/c
ID   ADQ32655 standard; DNA; 11 BP.
XX
AC   ADQ32655;
XX
DT   23-SEP-2004  (first entry)
XX
DE   Human facial skin-associated DNA fragment SEQ ID NO 745.
XX
KW   facial skin; human; serial analysis of gene expression; SAGE;
KW   homeostasis; biochip; cosmetic; pharmaceutical; ds.
XX
OS   Homo sapiens.
XX
PN   DE10260928-A1.
XX
PD   08-JUL-2004.
XX
PF   20-DEC-2002; 2002DE-01060928.
XX
PR   20-DEC-2002; 2002DE-01060928.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Schlotmann K,  Gassenmeier T,  Holtkoetter O;
PI   Conradt M,  Hofmann K;
XX
DR   WPI; 2004-518855/50.
XX
PT   In vitro identification of genes important for facial skin, useful for
PT   assessing homeostasis and in screening for pharmaceutical or cosmetic
PT   agents, based on differential expression analysis.
XX
PS   Claim 5; SEQ ID NO 745; 577pp; German.
XX
CC   This invention describes a novel in vitro method for identifying genes
CC   that are significant for facial skin in humans. The method comprises
CC   recovering, from facial skin, a first mixture of genetically expressed
CC   (transcribed and optionally translated) factors (i.e. proteins, mRNA or
CC   their fragments), recovering a second, similar mixture from some other
CC   human tissue, preferably skin from a protected area, especially from the
CC   breast and subjecting the mixtures to serial analysis of gene expression
CC   (SAGE) to identify those genes for which expression is markedly different
CC   between facial skin and the other tissue. The invention also describes an
CC   in vitro method for determining homeostasis of human facial skin; a test
CC   kit which comprises a solid support (flexible or rigid) on which are
CC   immobilised probes that bind specifically to the factors of interest and
CC   a biochip for determining homeostasis of human facial skin. The products
CC   of the invention are also used in a method which determines activity of
CC   cosmetic and pharmaceutical agents for use against disorders or
CC   disturbances of the homeostasis of human skin and a screening method for
CC   identifying cosmetic and pharmaceutical agents. The method allows
CC   identification of as many as possible of the genes important for facial
CC   skin and thus of a very wide range of potential therapeutic and cosmetic
CC   agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to
CC   identify the facial skin-associated genes described in the invention.
XX
SQ   Sequence 11 BP; 5 A; 3 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 30;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TTGTCTCCAGT 11
              |||||| ||||
Db         11 TTGTCTGCAGT 1


RESULT 22
AAZ81653
ID   AAZ81653 standard; DNA; 10 BP.
XX
AC   AAZ81653;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #887.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 82; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
```

```
SQ   Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 U; 0 Other;

  Query Match            45.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 31;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 TCCAGTCTC 14
              |||||||||
Db          2 TCCAGTCTC 10


RESULT 23
AAF42075
ID   AAF42075 standard; DNA; 10 BP.
XX
AC   AAF42075;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8814.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 314; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 1 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match            45.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 31;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 AGTCTCTTC 17
              |||||||||
Db          2 AGTCTCTTC 10


RESULT 24
ADU19570/c
ID   ADU19570 standard; DNA; 10 BP.
XX
AC   ADU19570;
XX
DT   13-JAN-2005  (first entry)
XX
DE   Hypoxia-related tumourigenesis-related SAGE tag #1361.
XX
KW   screening; hypoxia-related tumourigenesis;
KW   hypoxia-induced gene regulation; tumour; SAGE tag; ds.
XX
OS   Unidentified.
XX
PN   WO2004092198-A2.
XX
PD   28-OCT-2004.
XX
PF   09-APR-2004; 2004WO-US011087.
XX
PR   09-APR-2003; 2003US-0461712P.
XX
PA   (GENZ ) GENZYME CORP.
XX
PI   Nacht M;
XX
DR   WPI; 2004-758333/74.
XX
PT   Identifying agents that alter biological activity of a polypeptide
PT   encoded by a polynucleotide involved in hypoxia-related tumorigenesis
PT   comprises contacting an agent with a target cell and monitoring activity
PT   of expressed product.
XX
PS   Disclosure; Page 82; 100pp; English.
XX
CC   The invention comprises a method of screening for candidate agents
CC   capable of altering the biological activity of a protein encoded by a
CC   nucleotide involved in hypoxia-related tumourigenesis. The method of the
CC   invention involves: contacting a test agent with a target cell expressing
CC   the nucleotide, and monitoring the activity of the expressed protein
CC   product; if the test agent modifies the activity of the expressed protein
CC   then this is a candidate agent. The method of the invention is useful for
CC   modifying hypoxia-induced gene regulation and for diagnosing, prognosing
CC   or treating tumours. The present DNA sequence represents a SAGE tag that
CC   was used in the exemplification of the invention.
XX
SQ   Sequence 10 BP; 4 A; 1 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match            45.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 31;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 AGTCTCTTC 17
              |||||||||
Db         10 AGTCTCTTC 2


RESULT 25
```

```
ABQ87397/c
ID   ABQ87397 standard; cDNA; 11 BP.
XX
AC   ABQ87397;
XX
DT   10-SEP-2002  (first entry)
XX
DE   Human skin stress/ageing related EST SEQ ID NO 1152.
XX
KW   Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253773-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015178.
XX
PR   03-JAN-2001; 2001DE-01000121.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-528865/56.
XX
PT   Identifying genes involved in skin stress and aging, useful e.g. in
PT   screening for cosmetic or therapeutic agents, based on differential gene
PT   expression.
XX
PS   Claim 8; Page 85; 325pp; German.
XX
CC   The invention relates to identifying (M1) genes in vitro that, in humans
CC   or animals, are important for skin ageing and/or skin stress by serial
CC   analysis of gene expression between mixtures of transcribed and
CC   optionally translated, genetically encoded factors (A) obtained from
CC   young and aged skin, to identify that genes that show strong differential
CC   expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC   useful for: identifying markers of skin ageing and/or stress; determining
CC   skin ageing and/or stress; and identifying or determining the effects of
CC   pharmaceutical or cosmetic agents for control of skin ageing. The present
CC   sequence is one of a group of human skin ageing/stress related expressed
CC   sequence tags (ABQ86246-ABQ87680) of the invention
XX
SQ   Sequence 11 BP; 4 A; 1 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 AGTCTCTTC 17
              |||||||||
Db         10 AGTCTCTTC 2


RESULT 26
ABV70379/c
ID   ABV70379 standard; cDNA; 11 BP.
XX
AC   ABV70379;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 8165.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Claim 24; Page 261; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 3 A; 4 C; 3 G; 1 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TGTCTCCAG 10
              |||||||||
Db         11 TGTCTCCAG 3


RESULT 27
ABV62958/c
ID   ABV62958 standard; cDNA; 11 BP.
XX
AC   ABV62958;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 744.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
```

PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 45; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 3 A; 4 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGTCTCCAG 10
|||||||||
Db 11 TGTCTCCAG 3

RESULT 28
ABV69205
ID ABV69205 standard; cDNA; 11 BP.
XX
AC ABV69205;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 6991.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 219; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 2 A; 4 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGTCTCCAG 10
|||||||||
Db 3 TGTCTCCAG 11

RESULT 29
ABV66235
ID ABV66235 standard; cDNA; 11 BP.
XX
AC ABV66235;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 4021.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 136; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 1 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGTCTCCAG 10

```
              |||||||||
Db          3 TGTCTCCAG 11


RESULT 30
ABV65400/c
ID   ABV65400 standard; cDNA; 11 BP.
XX
AC   ABV65400;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 3186.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 113; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 4 A; 1 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 AGTCTCTTC 17
              |||||||||
Db         10 AGTCTCTTC 2


RESULT 31
ADG64354/c
ID   ADG64354 standard; DNA; 11 BP.
XX
AC   ADG64354;
XX
DT   11-MAR-2004  (first entry)
XX
DE   DNA polymerase 3'-5' exonuclease domain related PCR primer SEQ ID NO:39.
XX
KW   thermostable DNA polymerase; thermoactive DNA polymerase;
KW   3'-5' exonuclease domain; mutagenesis; genetic engineering;
KW   genetic fingerprinting; forensic; cloning; infectious agent;
KW   genetic disease; DNA polymerase; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   EP1350841-A2.
XX
PD   08-OCT-2003.
XX
PF   31-MAR-2003; 2003EP-00006888.
XX
PR   02-APR-2002; 2002US-0369815P.
XX
PA   (HOFF ) ROCHE DIAGNOSTICS GMBH.
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Schoenbrunner NJ,  Myers TW,  Gelfland DH;
XX
DR   WPI; 2003-815070/77.
XX
PT   New thermostable or thermoactive DNA polymerases with attenuated 3'-5'
PT   exonuclease activity, useful in polymerase chain reaction for in vitro
PT   mutagenesis and engineering of DNA, or genetic fingerprinting of forensic
PT   samples.
XX
PS   Example 1; SEQ ID NO 39; 80pp; English.
XX
CC   The present invention describes an isolated thermostable or thermoactive
CC   DNA polymerase. The DNA polymerase comprises: (a) a 3'-5' exonuclease
CC   domain which exhibits an attenuated 3'-5' exonuclease activity of about
CC   6.5 or less, but greater than 0, u/pmol, measured using the Standard
CC   Assay; or (b) a 3'-5' exonuclease domain, and having a 5'-3' polymerase
CC   activity and an attenuated 3'-5' exonuclease activity, where the ratio of
CC   the 5'-3' polymerase activity in u/pmol to the 3'-5' exonuclease activity
CC   in u/pmol is about 100-1. The thermostable or thermoactive DNA
CC   polymerases are useful in recombinant DNA techniques or polymerase chain
CC   reaction for in vitro mutagenesis and engineering of DNA, genetic
CC   fingerprinting of forensic samples, direct cloning from genomic DNA or
CC   cDNA, assays for the presence of infectious agents, or parental diagnosis
CC   of genetic disease. The DNA polymerase provides a significant improvement
CC   over thermostable or thermoactive DNA polymerases of prior art. The
CC   present DNA polymerases reduce degradation of primers as compared to wild
CC   type thermostable or thermoactive DNA polymerases. The DNA polymerases
CC   can be easily and efficiently expressed to a high level in a recombinant
CC   expression system, which facilitates commercial production of the enzyme,
CC   and they readily incorporate nucleoside triphosphate analogues, in
CC   contrast to thermostable archae proofreading DNA polymerase. The present
CC   sequence is used in the exemplification of the present invention.
XX
SQ   Sequence 11 BP; 5 A; 2 C; 4 G; 0 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          11 TCTCTTCGT 19
               |||||||||
Db          11 TCTCTTCGT 3


RESULT 32
ADR36038/c
ID   ADR36038 standard; DNA; 9 BP.
XX
AC   ADR36038;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Human nicking agent DNA containing BstNBI restriction site #2458.
XX
```

KW ss; nicking agent; assay panel; diagnosis; expression pattern;
KW DNA fingerprinting; nosocomial infection; microbiological assay;
KW bacterial contamination; genome mapping; bioremediation.
XX
OS Homo sapiens.
XX
PN WO2004067765-A2.
XX
PD 12-AUG-2004.
XX
PF 29-JAN-2004; 2004WO-US002720.
XX
PR 29-JAN-2003; 2003US-0443811P.
XX
PA (KECK-) KECK GRADUATE INST.
XX
PI Van Ness J, Galas DJ, Van Ness LK;
XX
DR WPI; 2004-581010/56.
XX
PT Identifying nucleic acid sample source, useful for identifying bacterial
PT strains involved in nosocomial infections, comprises treating the nucleic
PT acid sample with components comprising a nicking agent under nicking
PT conditions.
XX
PS Example 3; Page 105-219; 238pp; English.
XX
CC The invention relates to a method of treating a nucleic acid sample with
CC components under nicking conditions, where the components comprise a
CC nicking agent, and the conditions cause the nicking agent to nick the
CC nucleic acid sample to thus produce a family of initiating
CC oligonucleotide fragments, and subjecting one or more members of the
CC family of initiating oligonucleotide fragments to a characterization
CC process to thus provide results. The method is useful for creating an
CC assay panel of diagnostic oligonucleotides that can identify any organism
CC or individual. The method is useful for characterizing other DNA
CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
CC The method, kit or composition is useful for identifying the source
CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC non-human animal or human. The method is particularly useful for rapidly
CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,
CC subspecies, and especially strains or individuals of the subspecies. It
CC is especially useful for identifying different bacterial strains involved
CC in e.g., nosocomial infections. Furthermore, the method is useful for
CC diagnosing bacterial disease in plants and humans, monitoring for
CC bacterial content and/or contamination in the environment, monitoring
CC food for bacterial contamination, monitoring manufacturing processes for
CC bacterial contamination, monitoring quality assurance/quality control of
CC laboratory tests involving microbiological assays, tracing bacterial
CC contamination and/or outbreaks of bacterial infections, genome mapping,
CC monitoring bioremediation sites, and for monitoring agricultural sites
CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-
CC ADR37496 correspond to target nucleic acids containing an NBstNBI
CC restriction site and used in the method of the invention.
XX
SQ Sequence 9 BP; 4 A; 1 C; 2 G; 1 T; 0 U; 1 Other;

Query Match 43.0%; Score 8.6; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CAGTCTCTT 16
||||||:||
Db 9 CAGTCTSTT 1

RESULT 33
ADR36039/c
ID ADR36039 standard; DNA; 9 BP.
XX
AC ADR36039;
XX
DT 04-NOV-2004 (first entry)
XX
DE Human nicking agent DNA containing BstNBI restriction site #2459.
XX
KW ss; nicking agent; assay panel; diagnosis; expression pattern;
KW DNA fingerprinting; nosocomial infection; microbiological assay;
KW bacterial contamination; genome mapping; bioremediation.
XX
OS Homo sapiens.
XX
PN WO2004067765-A2.
XX
PD 12-AUG-2004.
XX
PF 29-JAN-2004; 2004WO-US002720.
XX
PR 29-JAN-2003; 2003US-0443811P.
XX
PA (KECK-) KECK GRADUATE INST.
XX
PI Van Ness J, Galas DJ, Van Ness LK;
XX
DR WPI; 2004-581010/56.
XX
PT Identifying nucleic acid sample source, useful for identifying bacterial
PT strains involved in nosocomial infections, comprises treating the nucleic
PT acid sample with components comprising a nicking agent under nicking
PT conditions.
XX
PS Example 3; Page 105-219; 238pp; English.
XX
CC The invention relates to a method of treating a nucleic acid sample with
CC components under nicking conditions, where the components comprise a
CC nicking agent, and the conditions cause the nicking agent to nick the
CC nucleic acid sample to thus produce a family of initiating
CC oligonucleotide fragments, and subjecting one or more members of the
CC family of initiating oligonucleotide fragments to a characterization
CC process to thus provide results. The method is useful for creating an
CC assay panel of diagnostic oligonucleotides that can identify any organism
CC or individual. The method is useful for characterizing other DNA
CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
CC The method, kit or composition is useful for identifying the source
CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC non-human animal or human. The method is particularly useful for rapidly
CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,
CC subspecies, and especially strains or individuals of the subspecies. It
CC is especially useful for identifying different bacterial strains involved
CC in e.g., nosocomial infections. Furthermore, the method is useful for
CC diagnosing bacterial disease in plants and humans, monitoring for
CC bacterial content and/or contamination in the environment, monitoring
CC food for bacterial contamination, monitoring manufacturing processes for
CC bacterial contamination, monitoring quality assurance/quality control of
CC laboratory tests involving microbiological assays, tracing bacterial
CC contamination and/or outbreaks of bacterial infections, genome mapping,
CC monitoring bioremediation sites, and for monitoring agricultural sites
CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-
CC ADR37496 correspond to target nucleic acids containing an NBstNBI
CC restriction site and used in the method of the invention.
XX
SQ Sequence 9 BP; 4 A; 1 C; 2 G; 1 T; 0 U; 1 Other;

Query Match 43.0%; Score 8.6; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CAGTCTCTT 16
||||||:||
Db 9 CAGTCTSTT 1

RESULT 34
ADR36041/c
ID ADR36041 standard; DNA; 9 BP.
XX

```
AC   ADR36041;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Human nicking agent DNA containing BstNBI restriction site #2461.
XX
KW   ss; nicking agent; assay panel; diagnosis; expression pattern;
KW   DNA fingerprinting; nosocomial infection; microbiological assay;
KW   bacterial contamination; genome mapping; bioremediation.
XX
OS   Homo sapiens.
XX
PN   WO2004067765-A2.
XX
PD   12-AUG-2004.
XX
PF   29-JAN-2004; 2004WO-US002720.
XX
PR   29-JAN-2003; 2003US-0443811P.
XX
PA   (KECK-) KECK GRADUATE INST.
XX
PI   Van Ness J,  Galas DJ,  Van Ness LK;
XX
DR   WPI; 2004-581010/56.
XX
PT   Identifying nucleic acid sample source, useful for identifying bacterial
PT   strains involved in nosocomial infections, comprises treating the nucleic
PT   acid sample with components comprising a nicking agent under nicking
PT   conditions.
XX
PS   Example 3; Page 105-219; 238pp; English.
XX
CC   The invention relates to a method of treating a nucleic acid sample with
CC   components under nicking conditions, where the components comprise a
CC   nicking agent, and the conditions cause the nicking agent to nick the
CC   nucleic acid sample to thus produce a family of initiating
CC   oligonucleotide fragments, and subjecting one or more members of the
CC   family of initiating oligonucleotide fragments to a characterization
CC   process to thus provide results. The method is useful for creating an
CC   assay panel of diagnostic oligonucleotides that can identify any organism
CC   or individual. The method is useful for characterizing other DNA
CC   molecules e.g., cDNA, and for characterizing cDNA expression patterns.
CC   The method, kit or composition is useful for identifying the source
CC   organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC   non-human animal or human. The method is particularly useful for rapidly
CC   fingerprinting DNA to identifying prokaryotic and eukaryotic species,
CC   subspecies, and especially strains or individuals of the subspecies. It
CC   is especially useful for identifying different bacterial strains involved
CC   in e.g., nosocomial infections. Furthermore, the method is useful for
CC   diagnosing bacterial disease in plants and humans, monitoring for
CC   bacterial content and/or contamination in the environment, monitoring
CC   food for bacterial contamination, monitoring manufacturing processes for
CC   bacterial contamination, monitoring quality assurance/quality control of
CC   laboratory tests involving microbiological assays, tracing bacterial
CC   contamination and/or outbreaks of bacterial infections, genome mapping,
CC   monitoring bioremediation sites, and for monitoring agricultural sites
CC   for test crops, bacteria and recombinant molecules. Sequences ADR33581-
CC   ADR37496 correspond to target nucleic acids containing an NBstNBI
CC   restriction site and used in the method of the invention.
XX
SQ   Sequence 9 BP; 4 A; 1 C; 2 G; 1 T; 0 U; 1 Other;

  Query Match             43.0%;  Score 8.6;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 2.5e+02;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CAGTCTCTT 16
              ||||||:||
Db          9 CAGTCTSTT 1


RESULT 35
ADR36040/c
ID   ADR36040 standard; DNA; 9 BP.
XX
AC   ADR36040;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Human nicking agent DNA containing BstNBI restriction site #2460.
XX
KW   ss; nicking agent; assay panel; diagnosis; expression pattern;
KW   DNA fingerprinting; nosocomial infection; microbiological assay;
KW   bacterial contamination; genome mapping; bioremediation.
XX
OS   Homo sapiens.
XX
PN   WO2004067765-A2.
XX
PD   12-AUG-2004.
XX
PF   29-JAN-2004; 2004WO-US002720.
XX
PR   29-JAN-2003; 2003US-0443811P.
XX
PA   (KECK-) KECK GRADUATE INST.
XX
PI   Van Ness J,  Galas DJ,  Van Ness LK;
XX
DR   WPI; 2004-581010/56.
XX
PT   Identifying nucleic acid sample source, useful for identifying bacterial
PT   strains involved in nosocomial infections, comprises treating the nucleic
PT   acid sample with components comprising a nicking agent under nicking
PT   conditions.
XX
PS   Example 3; Page 105-219; 238pp; English.
XX
CC   The invention relates to a method of treating a nucleic acid sample with
CC   components under nicking conditions, where the components comprise a
CC   nicking agent, and the conditions cause the nicking agent to nick the
CC   nucleic acid sample to thus produce a family of initiating
CC   oligonucleotide fragments, and subjecting one or more members of the
CC   family of initiating oligonucleotide fragments to a characterization
CC   process to thus provide results. The method is useful for creating an
CC   assay panel of diagnostic oligonucleotides that can identify any organism
CC   or individual. The method is useful for characterizing other DNA
CC   molecules e.g., cDNA, and for characterizing cDNA expression patterns.
CC   The method, kit or composition is useful for identifying the source
CC   organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC   non-human animal or human. The method is particularly useful for rapidly
CC   fingerprinting DNA to identifying prokaryotic and eukaryotic species,
CC   subspecies, and especially strains or individuals of the subspecies. It
CC   is especially useful for identifying different bacterial strains involved
CC   in e.g., nosocomial infections. Furthermore, the method is useful for
CC   diagnosing bacterial disease in plants and humans, monitoring for
CC   bacterial content and/or contamination in the environment, monitoring
CC   food for bacterial contamination, monitoring manufacturing processes for
CC   bacterial contamination, monitoring quality assurance/quality control of
CC   laboratory tests involving microbiological assays, tracing bacterial
CC   contamination and/or outbreaks of bacterial infections, genome mapping,
CC   monitoring bioremediation sites, and for monitoring agricultural sites
CC   for test crops, bacteria and recombinant molecules. Sequences ADR33581-
CC   ADR37496 correspond to target nucleic acids containing an NBstNBI
CC   restriction site and used in the method of the invention.
XX
SQ   Sequence 9 BP; 4 A; 1 C; 2 G; 1 T; 0 U; 1 Other;

  Query Match             43.0%;  Score 8.6;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 2.5e+02;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CAGTCTCTT 16
              ||||||:||
Db          9 CAGTCTSTT 1
```

```
RESULT 36
AAV05484
ID   AAV05484 standard; DNA; 10 BP.
XX
AC   AAV05484;
XX
DT   01-MAY-1998  (first entry)
XX
DE   BsmAI restriction recognition site.
XX
KW   Amplification; nucleic acid sequence; SDA; recognition site;
KW   strand displacement amplification; restriction endonuclease;
KW   alpha-boronated deoxynucleoside triphosphate; BsaI;
KW   hemimodified restriction site; ds.
XX
OS   Synthetic.
XX
PN   US5702926-A.
XX
PD   30-DEC-1997.
XX
PF   22-AUG-1996;   96US-00701270.
XX
PR   22-AUG-1996;   96US-00701270.
XX
PA   (BECT ) BECTON DICKINSON CO.
XX
PI   Walker GT,  Fraiser MS;
XX
DR   WPI; 1998-076416/07.
XX
PT   Strand displacement amplification of nucleic acids - using alpha-
PT   boronated deoxy:nucleoside tri:phosphate to create nickable restriction
PT   site.
XX
PS   Disclosure; Col 6; 7pp; English.
XX
CC   A novel method for amplifying a target nucleic acid sequence by strand
CC   displacement amplification (SDA) comprises, amplifying the target
CC   sequence in an SDA reaction in which an alpha-boronated deoxynucleoside
CC   triphosphate is incorporated into a double stranded recognition site for
CC   a restriction endonuclease, e.g. the present sequence. This produces a
CC   hemimodified restriction site that is nicked by the restriction
CC   endonuclease during the SDA reaction. Most alpha-boronated dNTP will
CC   mimic a corresponding alpha-thiolated dNTP in essentially all respects as
CC   regards SDA, though amplification efficiency is reduced in SDA reactions
CC   optimised for alpha-thiolated dNTP
XX
SQ   Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 38;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAGTC 12
              ||||||| ||
Db          1 GTCTCCAATC 10


RESULT 37
AAZ78224/c
ID   AAZ78224 standard; DNA; 10 BP.
XX
AC   AAZ78224;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:652.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965924-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013800.
XX
PR   19-JUN-1998;   98US-0089833P.
PR   19-JUN-1998;   98US-0089844P.
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089878P.
PR   19-JUN-1998;   98US-0089991P.
PR   19-JUN-1998;   98US-0089992P.
PR   19-JUN-1998;   98US-0089993P.
PR   19-JUN-1998;   98US-0089994P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0089999P.
PR   19-JUN-1998;   98US-0090000P.
PR   19-JUN-1998;   98US-0090035P.
PR   19-JUN-1998;   98US-0090036P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
PR   19-JUN-1998;   98US-0090042P.
PR   19-JUN-1998;   98US-0090043P.
PR   19-JUN-1998;   98US-0090044P.
PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer.
XX
PS   Claim 1; Page 84; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
CC   with monocytes. Some of the transcripts correspond to known genes or ESTs
CC   (expressed sequence tags) which were previously unknown to be
CC   preferentially or differentially expressed in dendritic cells, while
CC   other transcripts correspond to novel genes. Antigen-presenting cell
CC   (APC)-associated costimulatory factors play an important role in the
CC   activation of the cytotoxic immune response, particularly against tumour
CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
CC   complex) and subsequent recognition by T-cell receptors is alone
CC   insufficient to activate a robust cytotoxic immune response that can lyse
CC   the tumour cells, immunostimulatory cofactors also being required for
CC   efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC   sequences identified using the SAGE tags have several potential uses.
CC   They may be used in vaccines to induce an immune response, particularly
CC   against a tumour antigen; to modulate the genotype of an APC; to screen
CC   for agents that modulate expression of differentially expressed genes in
```

```
CC   an APC; and as hybridisation probes/amplification primers for the
CC   diagnosis, prognosis and monitoring of diseases related to abnormal
CC   expression of these genes. Detection of the dendritic cell differentially
CC   expressed genes, or of their encoded proteins, can be used to identify
CC   cells as belonging to the monocyte lineage. Cells containing these genes
CC   can be used in active immunotherapy (or to stimulate production of a
CC   population of antigen-specific effector cells) and vectors containing
CC   them are used in gene therapy. Co-administration of tumour antigens and
CC   APC-associated costimulatory factors ensures adequate antigen
CC   presentation to endogenous APCs and upregulates the APCs for the
CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells
XX
SQ   Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 38;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TGTCTCCAGT 11
              || |||||||
Db         10 TGGCTCCAGT 1


RESULT 38
AAZ82947/c
ID   AAZ82947 standard; DNA; 10 BP.
XX
AC   AAZ82947;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #2181.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 118; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 38;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCTCCAGTCT 13
              ||||||| ||
Db         10 TCTCCAGGCT 1


RESULT 39
AAZ83008
ID   AAZ83008 standard; DNA; 10 BP.
XX
AC   AAZ83008;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #2242.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 119; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
```

CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effecter
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 TCCAGTCTCT 15
||||| ||||
Db 1 TCCAGGCTCT 10

RESULT 40
AAZ86119/c
ID AAZ86119 standard; DNA; 10 BP.
XX
AC AAZ86119;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #5353.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 200; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effecter
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CTCCAGTCTC 14
||| ||||||
Db 10 CTCAAGTCTC 1

RESULT 41
AAS04430/c
ID AAS04430 standard; DNA; 10 BP.
XX
AC AAS04430;
XX
DT 07-SEP-2001 (first entry)
XX
DE Human DAXX DNA primer-extension oligonucleotide #17.
XX
KW Death-associated protein 6; DAXX; polymorphism; haplotype pair; human;
KW immune disorder; autoimmune disease; population diversity; ss;
KW paternity testing; anthropological lineage; forensic application;
KW primer-extension oligonucleotide.
XX
OS Homo sapiens.
XX
PN WO200125245-A2.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US027487.
XX
PR 06-OCT-1999; 99US-0157909P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Chew A, Choi JY, Denton RR, Nandabalan K, Stephens JC;
XX
DR WPI; 2001-308220/32.
XX
PT New human death-associated protein 6 (DAXX) gene variants comprising 19
PT polymorphic sites useful in studying the effect of variation on the
PT biological activity of DAXX and in developing drugs targeting the
PT protein.
XX
PS Disclosure; Page 20; 97pp; English.
XX
CC Sequences AAS04414-AAS04451 represent primer-extension oligonucleotides
CC specific for a DNA encoding human death-associated protein 6 (DAXX). This
CC DNA may comprise one or more polymorphisms at specific nucleotide
CC positions to form one of nineteen possible polymorphic variants.

CC Associations between a trait and a genotype or a haplotype of the DAXX
CC gene can be identified by comparing the frequency of the genotype or
CC haplotype in a population exhibiting the trait with that of a reference
CC population. A higher frequency in the trait population indicates an
CC association. Methods involving genotyping or haplotyping of the DAXX gene
CC of an individual can lead to prediction of haplotype pairs for the DAXX
CC gene of related individuals, and may be useful in studying the expression
CC and biological function of DAXX, as well as in developing drugs targeting
CC this protein. Polymorphic variants of DAXX are useful in studying the
CC effect of the variation on the biological activity of DAXX as well as on
CC the binding affinity of candidate drugs targeting DAXX for the treatment
CC of autoimmune diseases and other immune disorders. Polymorphism is also
CC useful for studying population diversity, anthropological lineage,
CC paternity testing, forensic applications, and for identifying
CC associations between the DAXX genetic variation and a trait such as level
CC of drug response or susceptibility to disease. DAXX proteins may be used
CC to measure binding affinities of one or more candidate drugs targeting
CC the DAXX protein
XX
SQ Sequence 10 BP; 4 A; 2 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CAGTCTCTTC 17
|||||||||
Db 10 CGGTCTCTTC 1

RESULT 42
AAF38748/c
ID AAF38748 standard; DNA; 10 BP.
XX
AC AAF38748;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5487.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 196; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 5 A; 1 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TCTCTTCGTT 20
||||| ||||
Db 10 TCTCTCCGTT 1

RESULT 43
AAF42997
ID AAF42997 standard; DNA; 10 BP.
XX
AC AAF42997;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11136.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 347; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes

CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 0 A; 4 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TCTCTTCGTT 20
|||| |||||
Db 1 TCTCCTCGTT 10

RESULT 44
AAF38731/c
ID AAF38731 standard; DNA; 10 BP.
XX
AC AAF38731;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5470.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 195; 419pp; English.
XX

CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 7 A; 1 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TCTCTTCGTT 20
||| ||||||
Db 10 TCTTTTCGTT 1

RESULT 45
AAF33728/c
ID AAF33728 standard; DNA; 10 BP.
XX
AC AAF33728;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:467.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.

```
XX
PS   Claim 1; Page 391; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 5 A; 0 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 38;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 CAGTCTCTTC 17
              || |||||||
Db         10 CATTCTCTTC 1


RESULT 46
AAF34179
ID   AAF34179 standard; DNA; 10 BP.
XX
AC   AAF34179;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:918.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 32; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 1 A; 3 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 38;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 TCCAGTCTCT 15
              || |||||||
Db          1 TCTAGTCTCT 10


RESULT 47
AAF39592/c
ID   AAF39592 standard; DNA; 10 BP.
XX
AC   AAF39592;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6331.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
```

```
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 226; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 3 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 38;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 TCCAGTCTCT 15
              ||||| ||||
Db         10 TCCAGCCTCT 1


RESULT 48
AAF38171
ID   AAF38171 standard; DNA; 10 BP.
XX
AC   AAF38171;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4910.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 175; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 38;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCTCCAGTCT 13
              || |||||||
Db          1 TCGCCAGTCT 10


RESULT 49
AAF39425/c
ID   AAF39425 standard; DNA; 10 BP.
XX
AC   AAF39425;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6164.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
```

XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 220; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 4 A; 3 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGTCTCCAGT 11
||||| ||||
Db 10 TGTCTGCAGT 1

RESULT 50
AAF41789/c
ID AAF41789 standard; DNA; 10 BP.
XX
AC AAF41789;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8528.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 304; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 4 A; 0 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CAGTCTCTTC 17
|| |||||||
Db 10 CACTCTCTTC 1

RESULT 51
AAF34632/c
ID AAF34632 standard; DNA; 10 BP.
XX
AC AAF34632;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1371.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.

XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 49; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 5 A; 0 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CAGTCTCTTC 17
|| |||||||
Db 10 CATTCTCTTC 1

RESULT 52
AAS98827/c
ID AAS98827 standard; DNA; 10 BP.
XX
AC AAS98827;
XX
DT 26-MAR-2002 (first entry)
XX
DE Colony stimulating factor 1 receptor (CSF1R) oligonucleotide #193.
XX
KW Colony stimulating factor 1 receptor; CSF1R; polymorphic variant;
KW cytostatic; gene therapy; malignant histiocytosis; isogene;
KW myeloid malignancy; inflammatory disorder; transgenic animal; haplotype;
KW genotype; human; allele specific oligonucleotide; ASO; primer;
KW primer extension; ss.
XX
OS Homo sapiens.
XX
PN WO200179225-A2.
XX
PD 25-OCT-2001.
XX
PF 12-APR-2001; 2001WO-US012044.
XX
PR 12-APR-2000; 2000US-0196411P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Chew A, Choi JY, Koshy B;
XX
DR WPI; 2002-075058/10.
XX
PT Novel polymorphic variants of colony stimulating factor 1 receptor useful
PT in studying expression and function of the protein, useful for screening
PT candidate drugs to treat diseases e.g. inflammatory disorders.
XX
PS Claim 17; Page 17; 164pp; English.
XX
CC The invention describes a novel isolated polynucleotide (I) comprising a
CC sequence which is a polymorphic variant (PV) of a reference sequence for
CC colony stimulating factor 1 receptor (CSF1R) gene, found on The
CC polypeptide are useful for improving the discovery and development of
CC drugs for treating diseases associated with CSF1R activity, e.g.,
CC malignant histiocytosis, myeloid malignancies, and inflammatory disorders
CC and the haplotypes can be used to validate CSF1R as a candidate target
CC for treating a specific condition or disease predicted to be associated
CC with CSF1R activity. Genotyping the CSF1R gene of an individual can also
CC be used in developing diagnostic tests and therapeutic treatments. (I) is
CC useful in studying the expression and function of CSF1R, and in
CC expressing CSF1R protein for use in screening for candidate drugs to
CC treat diseases related to CSF1R activity and in studying the effect of
CC the variation on the biological activity of CSF1R as well as on the
CC binding affinity of candidate drugs targeting CSF1R. Antibodies are
CC useful in a variety of diagnostic and prognostic formats and therapeutic
CC methods. A transgenic animal is useful in studying expression of the
CC CSF1R isogenes in vivo, for in vivo screening and testing of drugs
CC targeted against CSF1R protein, and for testing the efficacy of
CC therapeutic agents and compounds. Allele specific oligonucleotides (ASO)
CC are useful as probes and primers, and for assaying a polymorphism in the
CC target region. Without requiring any a priori knowledge of the phenotypic
CC effect of any particular CSF1R or haplotype the invention provides a
CC method for identifying lead compounds that are more likely to show
CC efficacy in clinical trials. This sequence is a primer used to detect
CC CSF1R gene polymorphisms by primer extension, described in the method of
CC the invention
XX
SQ Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GTCTCCAGTC 12
||||||| |
Db 10 GTCTCCAGGC 1

RESULT 53
ACC41713/c
ID ACC41713 standard; DNA; 10 BP.
XX
AC ACC41713;
XX
DT 21-MAY-2003 (first entry)
XX
DE Zinc finger protein DNA-binding domain target sequence SEQ ID NO:260.

XX
KW Zinc finger domain; zinc finger; zinc finger binding domain; probe;
KW chimeric nucleic acid; library; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO2003016571-A1.
XX
PD 27-FEB-2003.
XX
PF 17-AUG-2002; 2002WO-KR001560.
XX
PR 17-AUG-2001; 2001US-0313402P.
PR 22-APR-2002; 2002US-0374355P.
XX
PA (TOOL-) TOOLGEN INC.
XX
PI Kim J, Bae K, Park K, Kwon Y, Ryu E, Hwang M;
XX
DR WPI; 2003-268344/26.
XX
PT New library comprising polypeptides having zinc finger domains, useful
PT for producing chimeric nucleic acids.
XX
PS Claim 40; Page 105; 234pp; English.
XX
CC The present invention describes a library comprising polypeptides. Each
CC polypeptide comprises a first or second zinc finger domain. The domains
CC of each polypeptide are identical to a zinc finger domain from a
CC naturally occurring protein and either do not occur in the same naturally
CC occurring protein or occur in the same naturally occurring protein in a
CC different configuration than in the polypeptide. The domains vary among
CC polypeptides. Also described: (1) producing chimeric nucleic acids; (2)
CC generating an artificial zinc finger polypeptide that specifically binds
CC to a target DNA site; and (3) identifying a nucleic acid encoding a zinc
CC finger polypeptide that specifically recognises a target DNA site. The
CC library can be used for producing chimeric nucleic acids. ACC41551 to
CC ACC41758 and ABR40919 to ABR41015 represent nucleotide and amino acid
CC sequences given in the exemplification of the present invention
XX
SQ Sequence 10 BP; 5 A; 2 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 AGTCTCTTCG 18
||||||| |
Db 10 AGTCTCTTTG 1

RESULT 54
ADH69419
ID ADH69419 standard; DNA; 10 BP.
XX
AC ADH69419;
XX
DT 25-MAR-2004 (first entry)
XX
DE Exon 4/5 junction #2of Blue pigment gene.
XX
KW Human; Blue pigment gene; retina specific gene; ds; cancer; infection;
KW cytostatic; GAWTS; genomic amplification with transcript sequencing;
KW RAWTS; RNA amplification with transcript sequencing; tsRAWTS;
KW tissue specific RAWTS; RAWIT;
KW RNA amplification with in vitro translation; zooRAWTS; ASAWTS;
KW adjacent sequence amplification with transcript sequencing; PASA;
KW PCR amplification of specific alleles; PLATS;
KW promoter ligation with transcript sequencing.
XX
OS Homo sapiens.
XX
PN US2003143553-A1.
XX
PD 31-JUL-2003.
XX
PF 07-MAR-2002; 2002US-00094507.
XX
PR 28-JAN-1988; 88US-00149312.
PR 24-JUL-1989; 89US-00385013.
PR 12-NOV-1993; 93US-00151461.
PR 27-DEC-1994; 94US-00399855.
PR 22-FEB-2000; 2000US-00510177.
XX
PA (SOMM/) SOMMER S S.
XX
PI Sommer SS;
XX
DR WPI; 2003-730802/69.
XX
PT Amplifying a sequence of interest present within a nucleic acid molecule
PT for monitoring the progression of cancer by obtaining a sample of the
PT nucleic acid molecule and contacting the sample with an RNA polymerase.
XX
PS Disclosure; Fig 1B; 70pp; English.
XX
CC The invention relates to amplifying a sequence of interest present within
CC a nucleic acid molecule comprising: obtaining a sample of the nucleic
CC acid molecule that contains the sequence of interest; if the nucleic acid
CC is a single-stranded RNA molecule, treating the sample so as to prepare a
CC sample containing DNA molecule that contains a sequence complementary to
CC the sequence of interest; treating the sample to obtain a further sample;
CC contacting the further sample under hybridisation conditions with one
CC oligonucleotide primer that includes at least a promoter and a nucleic
CC acid present within the nucleic acid molecule, where the primer sequence
CC is located adjacent to, and 5′ of, the sequence of interest, so that the
CC oligonucleotide primer hybridises with the single-stranded DNA molecule;
CC treating the resulting sample containing the single stranded DNA molecule
CC to which the oligonucleotide primer is hybridised from step (4) with a
CC polymerase under polymerizing conditions so that a DNA extension product
CC of the oligonucleotide primer is synthesised and contains the sequence of
CC interest; treating the sample from step (5) so as to separate the DNA
CC extension product from the single-stranded DNA molecule on which it was
CC synthesised; contacting the resulting sample from step (6) containing the
CC sequence complementary to the sequence of interest under hybridisation
CC conditions, with one oligonucleotide primer; treating the sample
CC containing the single-stranded DNA molecule to which the oligonucleotide
CC primer is hybridised from step (7) with a polymerase so as to synthesise
CC a further DNA extension product; repeating steps (7)-(9), as desired;
CC contacting the sample from step (10) with an RNA polymerase that
CC initiates polymerization from the promoter present, under polymerising
CC conditions, so as to obtain multiple RNA transcripts of each DNA
CC extension product that contains the sequence complementary to the
CC sequence of interest. The promoter is a phage promoter, which is T7, T3
CC or SP6 promoter. The method (and its modifications detailed in the
CC specification are known as GAWTS (genomic amplification with transcript
CC sequencing), RAWTS (RNA amplification with transcript sequencing),
CC tsRAWTS (tissue specific RAWTS), RAWIT (RNA amplification with in vitro
CC translation), zooRAWTS (sequencing homologous genes across species)
CC ASAWTS (adjacent sequence amplification with transcript sequencing), PASA
CC (PCR amplification of specific alleles) and PLATS (promoter ligation with
CC transcript sequencing). The method is useful for amplifying a sequence of
CC interest present within a nucleic acid molecule for monitoring the
CC progression of cancer or the efficiency of treatment of cancer or for
CC diagnosing and subtyping infectious agents. The present sequence is a
CC human retina specific blue pigment gene exon 4/5 junction sequence
CC analysed by the method of the invention.
XX
SQ Sequence 10 BP; 1 A; 4 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTGTCTCCAG 10
|| |||||||

```
Db          1 TTCTCTCCAG 10


RESULT 55
ADP47134/c
ID   ADP47134 standard; DNA; 10 BP.
XX
AC   ADP47134;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human phospholipase A2-specific mAb heavy chain DNA sequence #14.
XX
KW   human; monoclonal antibody; phospholipase A2; PLA2;
KW   inflammatory disorder; degenerative disorder;
KW   joint inflammatory reaction; skin inflammatory reaction;
KW   blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
KW   Alzheimer's disease; atherosclerosis; restenosis; heavy chain; ds.
XX
OS   Homo sapiens.
XX
PN   WO2004050850-A2.
XX
PD   17-JUN-2004.
XX
PF   02-DEC-2003; 2003WO-US038234.
XX
PR   02-DEC-2002; 2002US-0430724P.
XX
PA   (ABGE-) ABGENIX INC.
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Landes GM,  Haak-Frendscho M,  Chen L,  Lee YR,  Liang ML,  Feng X;
PI   Jia X,  Nocerini MR;
XX
DR   WPI; 2004-461119/43.
XX
PT   New human monoclonal antibody that binds to phospholipase A2 (PLA2),
PT   useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
PT   asthma, Alzheimer's disease, atherosclerosis, or restenosis.
XX
PS   Example 5; SEQ ID NO 49; 128pp; English.
XX
CC   The invention comprises a human monoclonal antibody that binds to
CC   phospholipase A2 (PLA2). The monoclonal antibody of the invention is
CC   useful in the preparation of a medicament for the treatment of
CC   inflammatory and degenerative disorders stemming from inflammatory
CC   reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
CC   asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
CC   nucleic acid represents a human PLA2-specific monoclonal antibody heavy
CC   chain DNA sequence.
XX
SQ   Sequence 10 BP; 3 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 38;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 TCCAGTCTCT 15
              ||||||| ||
Db         10 TCCAGTCCCT 1


RESULT 56
ADZ67944/c
ID   ADZ67944 standard; DNA; 10 BP.
XX
AC   ADZ67944;
XX
DT   14-JUL-2005  (first entry)
XX
DE   NTRK1 gene polymorphic site 8 primer extension oligonucleotide.
XX
KW   Neurotrophic tyrosine kinase receptor type 1; NTRK1; Alzheimers disease;
KW   neurological disease; diagnosis; prognosis; primer; SNP detection;
KW   haplotype mapping; ss.
XX
OS   Homo sapiens.
XX
PN   WO2005037204-A2.
XX
PD   28-APR-2005.
XX
PF   14-OCT-2004; 2004WO-US033689.
XX
PR   15-OCT-2003; 2003US-0511247P.
XX
PA   (GENA-) GENAISSANCE PHARM.
XX
PI   Aerssens J,  Athanasiou M,  Brain C,  Cohen N,  Dain B,  Denton RR;
PI   Judson RS,  Ozdemir V,  Reed CR;
XX
DR   WPI; 2005-322749/33.
XX
PT   Determining whether individual has age of onset marker I or marker II, by
PT   determining whether individual has zero copies or copy of neurotrophic
PT   tyrosine kinase, receptor, type 1 haplotypes involved in onset of
PT   Alzheimer's disease.
XX
PS   Disclosure; SEQ ID NO 42; 128pp; English.
XX
CC   The inventors have discovered a set of 112 haplotypes in the human
CC   neurotrophic tyrosine kinase, receptor, type 1 (NTRK1) gene ADZ67903 that
CC   are associated with the age of onset of Alzheimer's disease (AD). They
CC   have also discovered that the copy number of each of these NTRK1
CC   haplotypes affects the age of onset of AD. If an individual has at least
CC   one copy of any of the 112 specified haplotypes, that individual is
CC   defined as having an 'age of onset marker I' and is more likely to have a
CC   later age of onset of AD than an individual having zero copies of any of
CC   the 112 haplotypes, such an individual being defined as 'age of onset
CC   marker II'. Testing for the presence or absence, and copy number, of the
CC   haplotypes is useful for predicting the age at which individuals who are
CC   at increased risk of AD are likely to develop AD and to help confirm a
CC   diagnosis of mild or minimal cognitive impairment (MDI) or AD. Such
CC   knowledge will assist therapy and lifestyle decisions. The correlation of
CC   certain NTRK1 haplotypes with age of AD onset indicates that variation in
CC   the NTKR1 gene should be considered in the development and clinical
CC   trials of drugs for treating MCI, AD and other neurodegenerative
CC   disorders. This correlation also provides a basis for pursuing NTRK1 as a
CC   target for drugs designed to treat cognitive disorders such as MDI, AD
CC   and other neurological diseases or conditions. Information is provided
CC   about the composition of each of 112 haplotypes, namely the location in
CC   the NTRK1 gene of each of the polymorphic sites (PSs) and the identity of
CC   the reference and variant allele at each PS. An individual's genotype for
CC   the set of PSs is obtained by primer extension, allele-specific PCR,
CC   nucleic acid amplification, hybridization, mismatch detection, enzymatic
CC   nucleic acid cleavage or sequencing assay. The present sequence is that
CC   of a reverse primer extension oligonucleotide for detecting PS8 in
CC   haplotypes comprising preferred embodiments of age of onset markers I and
CC   II.
XX
SQ   Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 38;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 CTCCAGTCTC 14
              | ||||||||
Db         10 CCCCAGTCTC 1


RESULT 57
AEA62012/c
ID   AEA62012 standard; DNA; 10 BP.
XX
```

```
AC   AEA62012;
XX
DT   11-AUG-2005  (first entry)
XX
DE   NTRK1 gene polymorphic site 8 primer extension oligonucleotide.
XX
KW   NTRK1 gene; neurotrophic tyrosine kinase, receptor, type 1;
KW   Alzheimers disease; degeneration; neurological disease;
KW   haplotype mapping; prognosis; primer; ss; SNP detection.
XX
OS   Homo sapiens.
XX
PN   WO2005052180-A2.
XX
PD   09-JUN-2005.
XX
PF   22-NOV-2004; 2004WO-US038876.
XX
PR   24-NOV-2003; 2003US-0524636P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Aerssens J,  Athanasiou M,  Brain C,  Cohen N,  Dain B,  Denton RR;
PI   Judson RS,  Ozdemir V,  Reed CR;
XX
DR   WPI; 2005-418015/42.
XX
PT   Determining whether an individual has a progression marker I or
PT   progression marker II, useful for predicting an individual's progression
PT   of Alzheimer's disease, by determining whether the individual has any of
PT   the NTRK1 haplotypes.
XX
PS   Claim 40; SEQ ID NO 53; 108pp; English.
XX
CC   The present invention relates to genetic markers of the human
CC   neurotrophic tyrosine kinase, receptor, type 1 (NTRK1) gene AEA61960 that
CC   are associated with progression of Alzheimer's disease (AD). 12
CC   Polymorphic sites (PSs) have been discovered in the NTRK1 gene of
CC   Caucasian individuals with AD, and a set of 70 haplotypes having
CC   association with progression of AD have been identified. If an individual
CC   has 0 or 1 copy of any of haplotypes 1-41 and 67-70, or 0 copies of any
CC   of haplotypes 42-66, then that individual is defined as having a
CC   progression marker I and is more likely to exhibit a slower progression
CC   of AD than an individual having 2 copies of any of haplotypes 1-41 and 67
CC   -70, or at least 1 copy of any of haplotypes 42-66, such an individual
CC   being defined as having a progression marker II. Additional haplotypes
CC   may be identified that are in linkage disequilibrium with any of
CC   haplotypes 1-70, referred to as linked haplotypes and substitute
CC   haplotypes of any of haplotypes 1-70, in which one or more of the PSs in
CC   the original haplotype is substituted with another PS, where the allele
CC   at the substituted PS is in linkage disequilibrium with the allele at the
CC   substituting PS. The invention provides methods and kits for determining
CC   whether an individual has a progression marker I or a progression marker
CC   II. A method is also provided for predicting an individual's progression
CC   of AD. The individual is especially a Caucasian diagnosed as having a
CC   cognitive disorder. An individual's genotype for each PS may be obtained
CC   by primer extension, allele-specific PCR, nucleic acid amplification,
CC   hybridization, mismatch-detection, enzymatic nucleic acid cleavage or
CC   sequencing assay. The present sequence is a reverse primer extension
CC   oligonucleotide that can be used to detect the allele at PS8 of the NTRK1
CC   gene. The 3' terminus of the oligonucleotide is complementary to the
CC   nucleotide located immediately adjacent to the PS. The oligonucleotide is
CC   included in a claimed kit of the invention used to determine whether an
CC   individual has a progression marker I or progression marker II.
XX
SQ   Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 38;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 CTCCAGTCTC 14
              | ||||||||
Db          - ----10 CCCCAGTCTC 1


RESULT 58
AAT09601
ID   AAT09601 standard; DNA; 8 BP.
XX
AC   AAT09601;
XX
DT   25-MAR-2003  (revised)
DT   25-JUN-1996  (first entry)
XX
DE   3'-primer used for characterisation of human biological samples.
XX
KW   3'-primer; human; protein coding region; PCR primer kit;
KW   characterisation; biological samples; PCR amplification; indexing;
KW   identification; cloning; analysis; genes; genome mapping;
KW   disease diagnosis; ss.
XX
OS   Synthetic.
XX
PN   WO9531574-A1.
XX
PD   23-NOV-1995.
XX
PF   12-MAY-1995;   95WO-US006032.
XX
PR   16-MAY-1994;   94US-00242887.
XX
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
PI   Lopeznieto CE,  Nigam SK;
XX
DR   WPI; 1996-010958/01.
XX
PT   Characterisation of nucleotide sequences using primer pairs - by PCR
PT   amplification and indexing of amplification prods. w.r.t. primers used
PT   for genome mapping and disease diagnosis.
XX
PS   Disclosure; Page 19; 72pp; English.
XX
CC   The 5'-primers AAT09358-508, and the 3'-primers AAT09509-659, which
CC   target human protein coding regions, together comprise a PCR primer kit
CC   with 1361 possible primer pairs. The kit is used in a new method for the
CC   characterisation of nucleic acid sequences obtd. from human biological
CC   samples, which comprises PCR amplification and indexing of the prods.
CC   w.r.t the primer pair that hybridised to its delineating subsequences.
CC   The method may be used in the identification, cloning and analysis of
CC   genes, e.g. in genome mapping, and disease diagnosis. (Updated on 25-MAR-
CC   2003 to correct PI field.)
XX
SQ   Sequence 8 BP; 1 A; 3 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAG 10
              ||||||||
Db          1 GTCTCCAG 8


RESULT 59
AAT09436/c
ID   AAT09436 standard; DNA; 8 BP.
XX
AC   AAT09436;
XX
DT   25-MAR-2003  (revised)
DT   21-JUN-1996  (first entry)
XX
DE   5'-primer used for characterisation of human biological samples.
XX
```

KW 5'-primer; human; protein coding region; PCR primer kit;
KW characterisation; biological samples; PCR amplification; indexing;
KW identification; cloning; analysis; genes; genome mapping;
KW disease diagnosis; ss.
XX
OS Synthetic.
XX
PN WO9531574-A1.
XX
PD 23-NOV-1995.
XX
PF 12-MAY-1995; 95WO-US006032.
XX
PR 16-MAY-1994; 94US-00242887.
XX
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
XX
PI Lopeznieto CE, Nigam SK;
XX
DR WPI; 1996-010958/01.
XX
PT Characterisation of nucleotide sequences using primer pairs - by PCR
PT amplification and indexing of amplification prods. w.r.t. primers used
PT for genome mapping and disease diagnosis.
XX
PS Claim 5; Page 44; 72pp; English.
XX
CC The 5'-primers AAT09358-508, and the 3'-primers AAT09509-659, which
CC target human protein coding regions, together comprise a PCR primer kit
CC with 1361 possible primer pairs. The kit is used in a new method for the
CC characterisation of nucleic acid sequences obtd. from human biological
CC samples, which comprises PCR amplification and indexing of the prods.
CC w.r.t the primer pair that hybridised to its delineating subsequences.
CC The method may be used in the identification, cloning and analysis of
CC genes, e.g. in genome mapping, and disease diagnosis. (Updated on 25-MAR-
CC 2003 to correct PI field.)
XX
SQ Sequence 8 BP; 2 A; 2 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GTCTCCAG 10
||||||||
Db 8 GTCTCCAG 1

RESULT 60
AAA80951/c
ID AAA80951 standard; DNA; 8 BP.
XX
AC AAA80951;
XX
DT 24-NOV-2000 (first entry)
XX
DE A. thaliana primer walking octamer SEQ ID NO: 264.
XX
KW Primer walking; octamer; primer; DNA sequencing; PCR; ss.
XX
OS Arabidopsis thaliana.
XX
PN US6083695-A.
XX
PD 04-JUL-2000.
XX
PF 21-MAY-1997; 97US-00859954.
XX
PR 15-APR-1996; 96US-00632782.
XX
PA (UYHO-) UNIV HOUSTON.
PA (HARD/) HARDIN S H.
XX
PI Hardin PE, Hardin SH, Homayouni R;
XX
DR WPI; 2000-474852/41.
XX
PT Sequencing an unknown DNA molecule for the polymerase chain reaction and
PT other primer processes comprises primer walking of octamer
PT oligonucleotides.
XX
PS Example 8; Col 157-158; 161pp; English.
XX
CC This invention describes a novel method for sequencing an unknown DNA
CC molecule which comprises selecting a library primer from an octamer
CC oligonucleotide library consisting of 48 8-bp sequences and corresponding
CC complementary sequences, where the library primer is complementary to a
CC known sequence adjacent to the unknown sequence or is complementary to a
CC sequence in a known extension product. The method is useful for DNA
CC nucleotide sequencing, in PCR, and in other processes which make use of
CC primers. The octamers are used to identify coding sequences. Primer
CC walking using the octamer libraries is advantageous over other sequencing
CC methods because it does not require multiple cloning steps nor subsequent
CC template preparations, and it is a directed and methodical approach.
CC AAA80688-A81253 represent the octamer primers used in the primer walking
CC method of the invention
XX
SQ Sequence 8 BP; 4 A; 1 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GTCTCTTC 17
||||||||
Db 8 GTCTCTTC 1

RESULT 61
AAA80762/c
ID AAA80762 standard; DNA; 8 BP.
XX
AC AAA80762;
XX
DT 24-NOV-2000 (first entry)
XX
DE A. thaliana primer walking octamer SEQ ID NO: 75.
XX
KW Primer walking; octamer; primer; DNA sequencing; PCR; ss.
XX
OS Arabidopsis thaliana.
XX
PN US6083695-A.
XX
PD 04-JUL-2000.
XX
PF 21-MAY-1997; 97US-00859954.
XX
PR 15-APR-1996; 96US-00632782.
XX
PA (UYHO-) UNIV HOUSTON.
PA (HARD/) HARDIN S H.
XX
PI Hardin PE, Hardin SH, Homayouni R;
XX
DR WPI; 2000-474852/41.
XX
PT Sequencing an unknown DNA molecule for the polymerase chain reaction and
PT other primer processes comprises primer walking of octamer
PT oligonucleotides.
XX
PS Example 8; Col 63-64; 161pp; English.
XX
CC This invention describes a novel method for sequencing an unknown DNA
CC molecule which comprises selecting a library primer from an octamer
CC oligonucleotide library consisting of 48 8-bp sequences and corresponding

```
CC   complementary sequences, where the library primer is complementary to a
CC   known sequence adjacent to the unknown sequence or is complementary to a
CC   sequence in a known extension product. The method is useful for DNA
CC   nucleotide sequencing, in PCR, and in other processes which make use of
CC   primers. The octamers are used to identify coding sequences. Primer
CC   walking using the octamer libraries is advantageous over other sequencing
CC   methods because it does not require multiple cloning steps nor subsequent
CC   template preparations, and it is a directed and methodical approach.
CC   AAA80688-A81253 represent the octamer primers used in the primer walking
CC   method of the invention
XX
SQ   Sequence 8 BP; 4 A; 1 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTGTCTCC 8
              ||||||||
Db          8 TTGTCTCC 1


RESULT 62
AAA81188/c
ID   AAA81188 standard; DNA; 8 BP.
XX
AC   AAA81188;
XX
DT   24-NOV-2000  (first entry)
XX
DE   A. thaliana primer walking octamer SEQ ID NO: 501.
XX
KW   Primer walking; octamer; primer; DNA sequencing; PCR; ss.
XX
OS   Arabidopsis thaliana.
XX
PN   US6083695-A.
XX
PD   04-JUL-2000.
XX
PF   21-MAY-1997;   97US-00859954.
XX
PR   15-APR-1996;   96US-00632782.
XX
PA   (UYHO-) UNIV HOUSTON.
PA   (HARD/) HARDIN S H.
XX
PI   Hardin PE,  Hardin SH,  Homayouni R;
XX
DR   WPI; 2000-474852/41.
XX
PT   Sequencing an unknown DNA molecule for the polymerase chain reaction and
PT   other primer processes comprises primer walking of octamer
PT   oligonucleotides.
XX
PS   Claim 1; Col 277-278; 161pp; English.
XX
CC   This invention describes a novel method for sequencing an unknown DNA
CC   molecule which comprises selecting a library primer from an octamer
CC   oligonucleotide library consisting of 48 8-bp sequences and corresponding
CC   complementary sequences, where the library primer is complementary to a
CC   known sequence adjacent to the unknown sequence or is complementary to a
CC   sequence in a known extension product. The method is useful for DNA
CC   nucleotide sequencing, in PCR, and in other processes which make use of
CC   primers. The octamers are used to identify coding sequences. Primer
CC   walking using the octamer libraries is advantageous over other sequencing
CC   methods because it does not require multiple cloning steps nor subsequent
CC   template preparations, and it is a directed and methodical approach.
CC   AAA80688-A81253 represent the octamer primers used in the primer walking
CC   method of the invention
XX
SQ   Sequence 8 BP; 3 A; 1 C; 3 G; 1 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TCTCCAGT 11
              ||||||||
Db          8 TCTCCAGT 1


RESULT 63
AAQ88288
ID   AAQ88288 standard; DNA; 10 BP.
XX
AC   AAQ88288;
XX
DT   27-AUG-2003  (revised)
DT   12-DEC-1995  (first entry)
XX
DE   5'-target sequence 2 for detection of fruit species by PCR.
XX
KW   Polymerase chain reaction amplification; fruit juice; fruit pulp;
KW   species detection; apple; orange; grapefruit; RAPD technique; ss.
XX
OS   Citrus.
XX
PN   FR2711143-A1.
XX
PD   21-APR-1995.
XX
PF   13-OCT-1994;   94FR-00012235.
XX
PR   13-OCT-1993;   93GB-00021113.
XX
PA   (UKAG-) UK MIN AGRIC FISHERIES & FOOD.
XX
PI   Lindsey K,  Twell D;
XX
DR   WPI; 1995-157154/21.
XX
PT   Identifying species, variety etc. of fruits by PCR amplification - then
PT   comparing products with standards, also new test kits, primers and
PT   hybridisation probes, partic. to detect fraudulent use in food prodn.
XX
PS   Claim 7; Page 17; 20pp; French.
XX
CC   Primers have been identified which give useful results for identification
CC   of genus, species or variety of fruits (see AAQ88293-Q88298);
CC   amplification profiles are established using several of the primers,
CC   which are complementary to regions (see AAQ88287-Q88292) at the 5'-end of
CC   the target sequences which are amplified. Using the primers it was
CC   possible to distinguish between e.g. different varieties of Navel oranges
CC   and also between "red" apples and "Granny Smith" apples. (Updated on 27-
CC   AUG-2003 to correct OS field.)
XX
SQ   Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CTCCAGTC 12
              ||||||||
Db          2 CTCCAGTC 9


RESULT 64
AAQ88294/c
ID   AAQ88294 standard; DNA; 10 BP.
XX
AC   AAQ88294;
XX
DT   12-DEC-1995  (first entry)
XX
```

DE Primer sequence 8 for detection of fruit species by PCR.
XX
KW Polymerase chain reaction amplification; fruit juice; fruit pulp;
KW species detection; apple; orange; grapefruit; RAPD technique; ss.
XX
OS Synthetic.
XX
PN FR2711143-A1.
XX
PD 21-APR-1995.
XX
PF 13-OCT-1994; 94FR-00012235.
XX
PR 13-OCT-1993; 93GB-00021113.
XX
PA (UKAG-) UK MIN AGRIC FISHERIES & FOOD.
XX
PI Lindsey K, Twell D;
XX
DR WPI; 1995-157154/21.
XX
PT Identifying species, variety etc. of fruits by PCR amplification - then
PT comparing products with standards, also new test kits, primers and
PT hybridisation probes, partic. to detect fraudulent use in food prodn.
XX
PS Claim 8; Page 17; 20pp; French.
XX
CC Primers have been identified which give useful results for identification
CC of genus, species or variety of fruits (see AAQ88293-Q88298);
CC amplification profiles are established using several of the primers,
CC which are complementary to regions (see AAQ88287-Q88292) at the 5'-end of
CC the target sequences which are amplified. Using the primers it was
CC possible to distinguish between e.g. different varieties of Navel oranges
CC and also between "red" apples and "Granny Smith" apples
XX
SQ Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CTCCAGTC 12
||||||||
Db 9 CTCCAGTC 2

RESULT 65
AAV50258
ID AAV50258 standard; DNA; 10 BP.
XX
AC AAV50258;
XX
DT 21-OCT-1998 (first entry)
XX
DE Yeast tag for additional NORF chromosome 4 tag position 381712.
XX
KW Yeast; Saccharomyces cerevisiae; transcriptome; cell cycle; regulation;
KW eukaryotic cell; antifungal; SAGE tag; gene expression;
KW serial analysis of gene expression; probe; ss.
XX
OS Saccharomyces cerevisiae.
OS Synthetic.
XX
PN WO9832847-A2.
XX
PD 30-JUL-1998.
XX
PF 22-JAN-1998; 98WO-US001216.
XX
PR 23-JAN-1997; 97US-0035917P.
XX
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Velculescu VE, Vogelstein B, Kinzler KW;
XX
DR WPI; 1998-427943/36.
XX
PT Yeast transcriptome - useful for modulating eukaryotic cell, for
PT screening antifungal agents, and for identifying genes in cell cycle
PT progression.
XX
PS Claim 1; Page 26; 44pp; English.
XX
CC Yeast transcriptome is encoded by a DNA molecule comprising a yeast gene
CC involved in cell cycle progression selected from the group of
CC nonannotated ORF (NORF) genes. SAGE (serial analysis gene expression)
CC tags for highly expressed genes and NORF genes are given in AAV50051 to
CC AAV50345. The present invention describes: (1) a method of using yeast
CC genes to modulate the cell cycle which comprises administering to a cell
CC an isolated DNA molecule comprising a yeast gene which is involved in
CC cell cycle progression selected from differentially expressed genes (SAGE
CC tags given in AAV50051 to AAV50345); (2) a method for screening candidate
CC antifungal drugs which comprises contacting a test substance with a yeast
CC cell and monitoring expression of a yeast gene which is involved in cell
CC cycle progression; (3) a method of identifying human genes which are
CC involved in cell cycle progression which comprises hybridizing a probe
CC comprising at least 10 contiguous nucleotides of a yeast gene which is
CC differentially expressed between at least 2 phases selected from the log
CC phase, the S phase and the G2/M phase; and (4) a probe for ascertaining
CC the phase in the cell cycle, where the probe comprises at least 14
CC contiguous nucleotides of a NORF gene (SAGE tags given in AAV50051 to
CC AAV50345), or as an array of probes on a solid support
XX
SQ Sequence 10 BP; 1 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCTCCAGT 11
||||||||
Db 1 TCTCCAGT 8

RESULT 66
AAZ08343/c
ID AAZ08343 standard; DNA; 10 BP.
XX
AC AAZ08343;
XX
DT 13-OCT-1999 (first entry)
XX
DE Nilaparvata lugens Stal. rice PCR primer sequence #9.
XX
KW Nilaparvata lugens Stal; rice; detection; resistance; PCR marker; bph-2;
KW PCR primer; ss.
XX
OS Synthetic.
OS Nilaparvata lugens.
XX
PN JP11206376-A.
XX
PD 03-AUG-1999.
XX
PF 22-JAN-1998; 98JP-00010845.
XX
PR 22-JAN-1998; 98JP-00010845.
XX
PA (AICH-) AICHI KEN PREFECTURE.
XX
DR WPI; 1999-486354/41.
XX
PT Detection of resistance to Nilaparvata lugens Stal. rice - using
PT amplification techniques.
XX
PS Example; Page 11; 15pp; Japanese.

```
XX
CC   A method has been developed for the detection of resistance to
CC   Nilaparvata lugens Stal. rice. The method comprises: (1) amplification of
CC   a DNA fragment by PCR using a PCR marker and detection of the resistance,
CC   in which a DNA fragment being specifically amplified in a species having
CC   a gene (bph-2) resistant to Nilaparvata lugens Stal. using a genome DNA
CC   of rice as a template and 1.3 Kbp in total with a base sequence shown by
CC   sequence 1 (AAZ08335), comprising 300 bases at 5'-terminal and sequence 2
CC   (AAZ08336) comprising 290 bases at 3'-terminal, respectively; and (2) a
CC   PCR marker comprising a sense primer of base numbers shown in sequence 3
CC   (AAZ08337) and an antisense primer of base numbers shown in sequence 5
CC   (AAZ08341). The present invention also describes a primer for PCR using
CC   rice genome of sequences 9, 10 or 11 (AAZ08343 to AAZ08345), or a couple
CC   of sense primer of sequences 3 or 7 (AAZ08341), respectively, for
CC   detection of the resistance. The method is used for the simple detection
CC   of resistance to Nilaparvata lugens Stal
XX
SQ   Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAG 10
              ||||||||
Db         10 GTCTCCAG 3


RESULT 67
AAZ81566
ID   AAZ81566 standard; DNA; 10 BP.
XX
AC   AAZ81566;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #800.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 79; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 2 A; 3 C; 2 G; 3 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 TCCAGTCT 13
              ||||||||
Db          2 TCCAGTCT 9


RESULT 68
AAZ86307/c
ID   AAZ86307 standard; DNA; 10 BP.
XX
AC   AAZ86307;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #5541.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 205; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
```

CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effecter
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GTCTCCAG 10
||||||||
Db 8 GTCTCCAG 1

RESULT 69
AAZ83592/c
ID AAZ83592 standard; DNA; 10 BP.
XX
AC AAZ83592;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #2826.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 134; 219pp; English.

XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effecter
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 4 A; 1 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCTCCAGT 11
||||||||
Db 10 TCTCCAGT 3

RESULT 70
AAZ85035
ID AAZ85035 standard; DNA; 10 BP.
XX
AC AAZ85035;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #4269.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.

```
XX
PS   Claim 1; Page 173; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 2 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TCTCCAGT 11
              ||||||||
Db          3 TCTCCAGT 10


RESULT 71
AAZ81791
ID   AAZ81791 standard; DNA; 10 BP.
XX
AC   AAZ81791;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #1025.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 86; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 3 A; 4 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CTCCAGTC 12
              ||||||||
Db          2 CTCCAGTC 9


RESULT 72
AAZ83176/c
ID   AAZ83176 standard; DNA; 10 BP.
XX
AC   AAZ83176;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #2410.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
```

```
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 124; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CCAGTCTC 14
              ||||||||
Db         10 CCAGTCTC 3


RESULT 73
AAZ80874/c
ID   AAZ80874 standard; DNA; 10 BP.
XX
AC   AAZ80874;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #108.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 61; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAG 10
              ||||||||
Db         10 GTCTCCAG 3


RESULT 74
AAC74005
ID   AAC74005 standard; cDNA; 10 BP.
XX
AC   AAC74005;
XX
DT   02-FEB-2001  (first entry)
XX
DE   Human dendritic cell cDNA base sequence oligonucleotide #92.
XX
KW   Human; dendritic cell; monocyte; immune system; diagnosis; cancer;
KW   autoimmune disease; tumour; ss.
XX
OS   Homo sapiens.
XX
PN   WO200060074-A1.
XX
PD   12-OCT-2000.
XX
PF   30-MAR-2000; 2000WO-JP002019.
XX
PR   01-APR-1999;   99JP-00095481.
XX
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI   Hashimoto S,  Matsushima K,  Suzuki T;
XX
DR   WPI; 2000-619172/59.
XX
PT   Groups of genes expressed in human dendritic cells at a greater or lesser
PT   extent than in monocytes for investigation and diagnosis of autoimmune
```

PT disease and tumors.
XX
PS Claim 1; Page 10; 95pp; Japanese.
XX
CC The present invention describes a group of genes consisting of 100 genes
CC which are highly expressed in human dendritic cells; a group of genes
CC which are expressed at a higher frequency in human dendritic cells than
CC in human monocytes; and a group of genes which are expressed at lower
CC frequency in human dendritic cells than in human monocytes. Each group of
CC genes are characterised in that cDNAs of these genes respectively have
CC the base sequences of SEQ ID NO:1 to 100 (AAC73914 to AAC74013), SEQ ID
CC NO:101 to 200 (AAC74014 to AAC74113) and SEQ ID NO:201 to 300 (AAC74114
CC to AAC74213), each is continuous with the base sequence 5'-CATG-3'
CC located most closely to the poly-A region. The sequences can be used for
CC the investigation of the role and mechanism of the involvement of
CC dendritic cells in the immune system and for the study and diagnosis of
CC diseases in which dendritic cells play a significant role, e.g. cancers
CC and autoimmune diseases
XX
SQ Sequence 10 BP; 2 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCTCCAGT 11
||||||||
Db 3 TCTCCAGT 10

RESULT 75
AAA56168
ID AAA56168 standard; DNA; 10 BP.
XX
AC AAA56168;
XX
DT 07-SEP-2000 (first entry)
XX
DE Human monocyte gene Tag oligonucleotide sequence SEQ ID NO:62.
XX
KW Human; monocyte; macrophage; GM-macrophage; M-macrophage; tag;
KW granulocyte-macrophage colony-stimulating factor; characterisation;
KW GM-CSF; identification; diagnosis; gene specificity; oncogenesis;
KW disease onset mechanism; genetic disease; drug development; ss.
XX
OS Homo sapiens.
XX
PN WO200024892-A1.
XX
PD 04-MAY-2000.
XX
PF 28-OCT-1999; 99WO-JP005982.
XX
PR 28-OCT-1998; 98JP-00307532.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Hashimoto S, Matsushima K, Suzuki T;
XX
DR WPI; 2000-350734/30.
XX
PT Genes most frequently expressed in human monocytes and GM-macrophages and
PT M-macrophages studied and with cDNAs characterized, for study of gene
PT specificity, disease onset mechanism, drug development and diagnosis.
XX
PS Claim 1; Page 51; 138pp; Japanese.
XX
CC The present invention describes 100 human genes, which are expressed most
CC frequently in human monocytes. The cDNA of each gene has a sequence fully
CC defined in the specification, and lacking the CATG sequence located
CC adjacent to polyA region. Also described are: (1) an antibody
CC specifically for the protein encoded by any of the genes; (2)
CC oligonucleotides obtained from the cDNA sequences; (3) 380 human genes
CC which are expressed most frequently in human macrophages, differentiated
CC from human monocytes by granulocyte-macrophage colony-stimulating factor,
CC the cDNA of each gene has a fully defined sequence, given in the
CC specification, lacking the base sequence CATG located most closely to the
CC poly A region; (4) an antibody specifically for the protein encoded by
CC any of the genes of (3); and (5) oligonucleotides obtained from the cDNA
CC sequences of (3). The genes and cDNAs, are used for the study of gene
CC specificity and disease onset mechanism e.g. oncogenesis, genetic
CC diseases, drug development and diagnosis. AAA56107 to AAA56586 represent
CC specifically claimed oligonucleotide tag sequences for human genes
CC expressed in monocytes and macrophages
XX
SQ Sequence 10 BP; 2 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCTCCAGT 11
||||||||
Db 3 TCTCCAGT 10

RESULT 76
AAA70756/c
ID AAA70756 standard; DNA; 10 BP.
XX
AC AAA70756;
XX
DT 17-JAN-2001 (first entry)
XX
DE PCR primer #2 for B. pumilus strain B3 DNA amplification.
XX
KW PCR primer; amplification; Bacillus pumilus B3; CECT 5105; plant growth;
KW Bacillus licheniformis B12; CECT 5106; gibberellin; plant hormone;
KW woody plant; herbaceous plant; disease resistance; ss.
XX
OS Bacillus pumilus.
XX
PN WO200043497-A1.
XX
PD 27-JUL-2000.
XX
PF 18-JAN-2000; 2000WO-ES000017.
XX
PR 20-JAN-1999; 99ES-00000106.
XX
PA (UYSA-) UNIV SAN PABLO CEU.
XX
PI Gutierrez Manero J, Probanza Lobo A;
XX
DR WPI; 2000-499226/44.
XX
PT New strains of Bacillus, useful for promoting growth of herbaceous and
PT woody plants, produce gibberellin plant hormones.
XX
PS Disclosure; Page 15; 28pp; Spanish.
XX
CC The invention relates to the isolation of novel strains of bacteria
CC (Bacillus pumilus B3 (CECT 5105) and B. licheniformis B12 (CECT 5106))
CC which produce gibberellin plant hormones that regulate plant growth. The
CC plant growth hormones are produced at level of 0.0029-0.148 mg/l by B3
CC and at 0.0017-0.123 mg/l by B12, after 24 hour culture at 28 deg. C in
CC liquid medium. The new strains are used to treat cultured plants (both
CC woody and herbaceous) to increase their growth, vigour and disease
CC resistance. Primers AAA70755-A70762 were used to PCR amplify DNA from the
CC B. pumilus strain B3
XX
SQ Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          5 CTCCAGTC 12
              ||||||||
Db          9 CTCCAGTC 2


RESULT 77
AAH63895
ID   AAH63895 standard; cDNA; 10 BP.
XX
AC   AAH63895;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 735.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US031922.
XX
PR   24-NOV-1999;   99US-00448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell type,
PT   such as cancer cell, comprises transcriptomes expressed in particular
PT   cell types.
XX
PS   Claim 13; Page 56; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences AAH63161-
CC   AAH64724 is expressed by the cell. The transcriptomes described in the
CC   invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of the
CC   transcriptomes described in the exemplification of the invention
XX
SQ   Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CAGTCTCT 15
              ||||||||
Db          1 CAGTCTCT 8


RESULT 78
AAH63530
ID   AAH63530 standard; cDNA; 10 BP.
XX
AC   AAH63530;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 370.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US031922.
XX
PR   24-NOV-1999;   99US-00448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell type,
PT   such as cancer cell, comprises transcriptomes expressed in particular
PT   cell types.
XX
PS   Claim 13; Page 47; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences AAH63161-
CC   AAH64724 is expressed by the cell. The transcriptomes described in the
CC   invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of the
CC   transcriptomes described in the exemplification of the invention
XX
SQ   Sequence 10 BP; 2 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TCTCCAGT 11
              ||||||||
Db          3 TCTCCAGT 10


RESULT 79
AAH41695/c
ID   AAH41695 standard; DNA; 10 BP.
XX
AC   AAH41695;
XX
DT   28-AUG-2001  (first entry)
XX
DE   Anti-PEP gene construction related oligonucleotide S4.
XX
KW   Phosphoenopyruvate carboxylase; PEPCase; seed; acetyl-CoA carboxylase;
KW   oilseed; PEP; plant breeding; soya bean; sunflower; rapeseed; peanut;
KW   sesame; crop plant; protein content; fatty acid content; anti-PEP; ss.
XX
OS   Synthetic.
XX
PN   WO200134812-A1.
XX
PD   17-MAY-2001.
XX
PF   06-NOV-2000; 2000WO-CN000418.
XX
PR   09-NOV-1999;   99CN-00124511.
XX
PA   (ZHEJ-) ZHEJIANG AGRIC SCI ACAD.
XX
PI   Chen J,  Lang C,  Huang R,  Hu Z,  Liu Z;
XX
DR   WPI; 2001-335934/35.
XX
```

```
PT   Altering protein/fatty acid composition of seeds, useful for producing
PT   e.g. soya bean or sesame seed with high protein/fatty acid content,
PT   comprises introducing antisense gene.
XX
PS   Example 8; Page 8; 25pp; Chinese.
XX
CC   The present invention describes a method for altering the protein/fatty
CC   acid composition of seeds. The method comprises: (1) cloning
CC   phosphoenopyruvate carboxylase (PEP) or acetyl-CoA carboxylase (ACC)
CC   genes or their fragments; (2) constructing the corresponding antisense
CC   gene of anti-PEP or anti-ACC; and (3) introducing the antisense gene into
CC   the plant cell of a crop. The method is applicable in plant breeding to
CC   give oilseed crops with high oil or protein content like soya bean,
CC   sunflower, rapeseed, peanut and sesame. The produced crop plants have
CC   high yield of oil or protein. The present sequence represents an
CC   oligonucleotide which is used in the construction of an anti-PEP gene in
CC   an example from the present invention
XX
SQ   Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CTCCAGTC 12
              ||||||||
Db          9 CTCCAGTC 2


RESULT 80
AAF69645/c
ID   AAF69645 standard; DNA; 10 BP.
XX
AC   AAF69645;
XX
DT   18-APR-2001  (first entry)
XX
DE   Human IL4Ralpha gene probe #285.
XX
KW   Polymorphism; human; interleukin 4 receptor-alpha; IL4R-alpha;
KW   allergic disease; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO200104270-A1.
XX
PD   18-JAN-2001.
XX
PF   13-JUL-2000; 2000WO-US019094.
XX
PR   13-JUL-1999;   99US-0143435P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Chew A,  Denton RR,  Duda A,  Nandabalan K,  Stephens JC;
PI   Windemuth AK;
XX
DR   WPI; 2001-103078/11.
XX
PT   New isolated polynucleotide useful for the identification of therapeutics
PT   in allergic diseases is new.
XX
PS   Disclosure; Page 46; 188pp; English.
XX
CC   The present invention relates to polymorphisms of the human interleukin 4
CC   receptor-alpha gene (IL4R-alpha; see AAF57718 for the reference
CC   sequence). Polynucleotides comprising polymorphic gene variants are
CC   useful for therapeutic purposes. For example, where a patient may benefit
CC   from expression of a particular IL4Ralpha protein isoform, an expression
CC   vector encoding the isoform may be administered to the patient. It may
CC   desirable to decrease or block expression of a particular IL4Ralpha
CC   isogene, which may be done by turning off by transforming a targeted
CC   organ, tissue or cell population with an expression vector that expresses
CC   high levels of untranslatable mRNA for the isogene. Specific therapeutics
CC   identified by these methods may be useful for allergic diseases. The
CC   present sequence is a probe for human IL4R-alpha
XX
SQ   Sequence 10 BP; 3 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TGTCTCCA 9
              ||||||||
Db          8 TGTCTCCA 1


RESULT 81
AAF38187
ID   AAF38187 standard; DNA; 10 BP.
XX
AC   AAF38187;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4926.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 175; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
```

CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 1 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCTCCAGT 11
||||||||
Db 1 TCTCCAGT 8

RESULT 82
AAF39032
ID AAF39032 standard; DNA; 10 BP.
XX
AC AAF39032;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5771.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 206; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 3 A; 3 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCTCCAGT 11
||||||||
Db 3 TCTCCAGT 10

RESULT 83
AAF36782
ID AAF36782 standard; DNA; 10 BP.
XX
AC AAF36782;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3521.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 125; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;

```
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 1 A; 2 C; 1 G; 6 T; 0 U; 0 Other;

  Query Match           40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 TCTTCGTT 20
               ||||||||
Db          1 TCTTCGTT 8


RESULT 84
AAF43826
ID   AAF43826 standard; DNA; 10 BP.
XX
AC   AAF43826;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11965.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 377; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 0 A; 3 C; 1 G; 6 T; 0 U; 0 Other;

  Query Match           40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GTCTCTTC 17
               ||||||||
Db          3 GTCTCTTC 10


RESULT 85
AAF41988/c
ID   AAF41988 standard; DNA; 10 BP.
XX
AC   AAF41988;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8727.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 311; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
```

CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 2 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCAGTCTC 14
||||||||
Db 8 CCAGTCTC 1

RESULT 86
AAF33475
ID AAF33475 standard; DNA; 10 BP.
XX
AC AAF33475;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:214.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Claim 1; Page 26; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 1 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCTCCAGT 11
||||||||
Db 1 TCTCCAGT 8

RESULT 87
AAF41634
ID AAF41634 standard; DNA; 10 BP.
XX
AC AAF41634;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8373.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 299; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes

```
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 0 A; 4 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTGTCTCC 8
              ||||||||
Db          3 TTGTCTCC 10


RESULT 88
AAS95346
ID   AAS95346 standard; DNA; 10 BP.
XX
AC   AAS95346;
XX
DT   14-FEB-2002  (first entry)
XX
DE   Human Histamine H2 receptor ASO primer extension PCR primer #6.
XX
KW   Human; histamine H2 receptor; HRH2; ss; PCR primer; polymorphic variant;
KW   haplotyping; genotyping; acid-peptic disorder; mammary cancer;
KW   gastric carcinoma; allele specific oligonucleotide; ASO;
KW   primer extension.
XX
OS   Homo sapiens.
XX
PN   WO200179220-A2.
XX
PD   25-OCT-2001.
XX
PF   12-APR-2001; 2001WO-US011941.
XX
PR   12-APR-2000; 2000US-0196406P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Chew A,  Choi JY,  Koshy B;
XX
DR   WPI; 2002-055249/07.
XX
PT   New human histamine H2 receptor (HRH2) isogene polymorphic variants,
PT   useful in expressing HRH2 protein for use in screening for candidate
PT   drugs to treat diseases related to HRH2 activity.
XX
PS   Claim 17; Page 14; 62pp; English.
XX
CC   The invention relates to an isolated polynucleotide comprising a
CC   polymorphic variant of a reference sequence for human Histamine H2
CC   receptor (HRH2) gene, its fragment or complement, and the polymorphic
CC   variant contains an HRH2 isogene defined by a haplotype listed in the
CC   specification. Also disclosed are methods for haplotyping and genotyping
CC   the HRH2 gene of an individual, a method for predicting a haplotype pair
CC   for the HRH2 gene of an individual, identifying an association between a
CC   trait and at least one haplotype or haplotype pair of HRH2 gene, allele
CC   specific oligonucleotides (ASO) for performing the haplotyping/
CC   genotyping, a recombinant nonhuman organisms transformed or transfected
CC   with the polymorphic variant, the protein expressed by the polymorphic
CC   variant, an antibody raised against the protein and screening for drugs
CC   targeting the polypeptide by contacting HRH2 polymorphic variant with a
CC   candidate agent and assaying for binding activity. The polymorphisms are
CC   useful for studying the biological function of HRH2 gene, as well as in
CC   identifying drugs targeting this protein for the treatment of disorder
CC   related to its abnormal expression or function. The polymorphic variants
CC   may be used in screening for compounds targeting CALM1 to treat a
CC   specific condition or disease predicted to be associated with HRH2
CC   activity, in studying the effect of the variation on the biological
CC   activity of HRH2 as well as on the binding affinity of candidate drugs
CC   targeting HRH2 for the treatment of acid-peptic disorders of the
CC   gastrointestinal tract and also possibly human mammary cancer and gastric
CC   carcinoma. The polymorphism and haplotype data can also be used for
CC   validating whether HRH2 is a suitable drug target for drugs to treat acid
CC   -peptic disorders of the gastrointestinal tract, screening of such drugs
CC   and reducing bias in clinical trials of such drugs. The present sequence
CC   is the 3' terminus of an ASO primer extension PCR primer used to detect
CC   the polymorphisms of the invention
XX
SQ   Sequence 10 BP; 1 A; 5 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CTCCAGTC 12
              ||||||||
Db          1 CTCCAGTC 8


RESULT 89
ABL60204
ID   ABL60204 standard; DNA; 10 BP.
XX
AC   ABL60204;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Human MUC1 PCR primer SEQ ID NO 48.
XX
KW   Human; mucin 1; MUC1; transmembrane protein; SNP; cancer; cytostatic;
KW   single nucleotide polymorphism; haplotyping; genotyping; drug;
KW   antiinflammatory; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200226765-A2.
XX
PD   04-APR-2002.
XX
PF   25-SEP-2001; 2001WO-US030151.
XX
PR   28-SEP-2000; 2000US-0236113P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Chew A,  Koshy B;
XX
DR   WPI; 2002-405042/43.
XX
PT   New genetic variants of mucin 1, Transmembrane gene, useful in studying
PT   expression and function of protein encoded by the gene and for screening
```

PT drugs to treat diseases e.g. cancer.
XX
PS Claim 16; Page 14; 75pp; English.
XX
CC The invention relates to a polynucleotide (ABL60158, ABL60159) encoding
CC mucin 1/MUC1 (ABB77476), Transmembrane isogene. The invention describes
CC novel genetic variants of the MUC1 gene. The invention is useful for
CC haplotyping/genotyping the MUC1 gene in an individual and identifying an
CC association between a trait and at least one of the haplotypes or
CC haplotype pairs of MUC1 gene. MUC1 is useful for studying the expression
CC and function of MUC1 and expressing MUC1 protein for use in screening for
CC candidate drugs to treat diseases related to MUC1 activity and in
CC studying the effect of the variation on the biological activity of MUC1
CC as well as on the binding affinity of candidate drugs targeting MUC1 for
CC the treatment of e.g. cancer. MUC1 is further used by the pharmaceutical
CC research scientist to validate MUC1 as a candidate target for and in
CC design of clinical trials of candidate drugs for, treating a specific
CC condition drugs or disease predicted to be associated with MUC1 activity.
CC MUC1 antibodies are useful in a variety of diagnostic and prognostic
CC formats and therapeutic methods. The present sequence is that of a PCR
CC primer for detecting MUC1 polymorphisms, useful to the invention
XX
SQ Sequence 10 BP; 1 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGTCTCCA 9
||||||||
Db 3 TGTCTCCA 10

RESULT 90
AAD25917
ID AAD25917 standard; DNA; 10 BP.
XX
AC AAD25917;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human MC4R gene polymorphism detecting primer #2.
XX
KW Human; single nucleotide polymorphism; SNP; melanocortin 4-receptor;
KW MC4R; haplotype; obesity; screening; allele-specific oligonucleotide;
KW ASO; gene therapy; anorectic; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200179222-A2.
XX
PD 25-OCT-2001.
XX
PF 12-APR-2001; 2001WO-US011943.
XX
PR 12-APR-2000; 2000US-0196677P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Bentivegna SC, Choi JY, Kazemi A, Lee HH, Nandabalan K, Parks KE;
PI Sausker EA;
XX
DR WPI; 2002-082744/11.
XX
PT Novel polymorphic variants of melanocortin 4-receptor gene useful in
PT studying expression and function of the protein, useful for screening
PT candidate drugs to treat diseases related to the protein activity e.g.
PT obesity.
XX
PS Claim 17; Page 13; 53pp; English.
XX
CC The invention relates to single nucleotide polymorphisms (SNP) in human
CC melanocortin 4-receptor (MC4R) gene. MC4R gene haplotypes are useful for
CC improving the efficiency and reliability of several steps in the
CC discovery and development of drugs for treating diseases associated with
CC MC4R activity, e.g. obesity. MC4R gene is useful in studying the
CC expression and function of MC4R and in expressing MC4R protein for use in
CC screening for candidate drugs to treat diseases related to MC4R activity
CC and in studying the effect of the variation on the biological activity of
CC MC4R as well as on the binding affinity of candidate drugs targetting
CC MC4R for the treatment of obesity. MC4R antibody is useful in a variety
CC of diagnostic and prognostic formats and in therapeutic methods. Allele-
CC specific oligonucleotide (ASO) is useful as probes and primers, and for
CC assaying a polymorphism in MC4R gene. MC4R DNA is used in gene therapy.
CC The present sequence is a primer used to detect polymorphism in human
CC MC4R gene
XX
SQ Sequence 10 BP; 1 A; 2 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AGTCTCTT 16
||||||||
Db 2 AGTCTCTT 9

RESULT 91
AAS95397/c
ID AAS95397 standard; DNA; 10 BP.
XX
AC AAS95397;
XX
DT 14-FEB-2002 (first entry)
XX
DE Human ICAM2 gene allele-specific oligonucleotide PCR primer #2.
XX
KW Human; intercellular adhesion molecule 2; ICAM2; haplotyping; ss;
KW haplotype pair; single nucleotide polymorphism; genotyping; PCR primer;
KW gene therapy; drug screening; anti-HIV; antiinflammatory; probe;
KW human immunodeficiency virus; sequencing primer.
XX
OS Homo sapiens.
XX
PN WO200185918-A1.
XX
PD 15-NOV-2001.
XX
PF 07-MAY-2001; 2001WO-US014714.
XX
PR 05-MAY-2000; 2000US-0201946P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Chew A, Choi JY, Denton RR, Kliem SE, Lee HH, Nandabalan K;
XX
DR WPI; 2002-055590/07.
XX
PT Novel polynucleotide containing polymorphisms in intercellular adhesion
PT molecule 2 gene, useful in developing drugs for treating human
PT immunodeficiency virus infection and inflammatory diseases.
XX
PS Claim 18; Page 13; 81pp; English.
XX
CC The invention relates to single nucleotide polymorphisms in the gene
CC encoding human intercellular adhesion molecule 2 (ICAM2). A method for
CC haplotyping the ICAM2 gene in an individual comprises identifying the
CC nucleotide at one or more polymorphic sites and determining whether one
CC of the copies of the gene is defined by one of the ICAM2 haplotypes given
CC in the specification or whether both copies are defined by a haplotype
CC pair. This method is useful in genotyping, whereby all possible haplotype
CC pairs can be assigned to specific genotypes. An association between a
CC trait and a haplotype or haplotype pair of the ICAM2 gene can be
CC identified by comparing the frequency of the haplotype or haplotype pair
CC in a population exhibiting the trait with the frequency of the haplotype

```
CC   or haplotype pair in a reference population, where a higher haplotype
CC   frequency in the trait population indicates the trait is associated with
CC   the haplotype or haplotype pair. ICAM2 and its corresponding DNA are used
CC   for studying the expression and function of ICAM2, for use in screening
CC   for candidate drugs to treat diseases related to ICAM2 activity, such as
CC   HIV infection and inflammatory diseases. The sequences are also useful
CC   for studying the effect of variation on the biological activity of ICAM2
CC   as well as on the binding affinity of candidate drugs targeting ICAM2.
CC   Sequences AAS95362-AAS95417 and AAS95419-AAS95442 represent allele-
CC   specific oligonucleotide probes, sequencing primers, PCR primers and cDNA
CC   encoding human ICAM2
XX
SQ   Sequence 10 BP; 4 A; 1 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTGTCTCC 8
              ||||||||
Db         10 TTGTCTCC 3


RESULT 92
ABV78460/c
ID   ABV78460 standard; cDNA; 10 BP.
XX
AC   ABV78460;
XX
DT   29-NOV-2002  (first entry)
XX
DE   Human Th1 cell preferentially expressed EST SAGE tag, SEQ ID NO:171.
XX
KW   SAGE tag; serial analysis of gene expression; human; Th1 cell;
KW   activated T cell; T lymphocyte; immune response; expression pattern;
KW   preferential expression; immune disorder; EST; expressed sequence tag;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   JP2002186482-A.
XX
PD   02-JUL-2002.
XX
PF   19-DEC-2000; 2000JP-00385816.
XX
PR   19-DEC-2000; 2000JP-00385816.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2002-594261/64.
XX
PT   Human activated Th1 and Th2 cell expression gene group, useful for the
PT   diagnosis and treatment of Th1 and Th2-related diseases.
XX
PS   Claim 19; Page 11; 60pp; Japanese.
XX
CC   The invention relates to SAGE (serial analysis of gene expression) tags
CC   representing groups of genes which are expressed in activated human Th1
CC   and/or Th2 cells. The SAGE tags of this invention consist of a sequence
CC   of 10 nucleotides located downstream of the 5'-CATG-3' sequence motif
CC   lying nearest to the polyA region of cDNAs derived from a variety of
CC   genes. These tags serve to uniquely identify each transcript and can thus
CC   be used to analyse the pattern of gene expression in particular cell
CC   types. The invention also relates to proteins encoded by the genes
CC   expressed in Th1 and/or Th2 cells, antibodies against these proteins, and
CC   inhibitors of the expression of groups of genes that are expressed in
CC   either or both the two cell types. Groups of genes expressed in Th1
CC   and/or Th2 cell types may be used for the diagnosis and treatment of Th1
CC   and Th2-related disorders. Sequences ABV78390-ABV78560 are SAGE tags
CC   representing 171 genes which are more highly expressed in Th1 cells
CC   compared with Th2 cells
XX
SQ   Sequence 10 BP; 4 A; 1 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 TCCAGTCT 13
              ||||||||
Db          8 TCCAGTCT 1


RESULT 93
ABV78336
ID   ABV78336 standard; cDNA; 10 BP.
XX
AC   ABV78336;
XX
DT   29-NOV-2002  (first entry)
XX
DE   Human ribosomal protein L23 SAGE tag, SEQ ID NO:47.
XX
KW   SAGE tag; serial analysis of gene expression; human; Th1 cell;
KW   activated T cell; T lymphocyte; immune response; expression pattern;
KW   immune disorder; ss.
XX
OS   Homo sapiens.
XX
PN   JP2002186482-A.
XX
PD   02-JUL-2002.
XX
PF   19-DEC-2000; 2000JP-00385816.
XX
PR   19-DEC-2000; 2000JP-00385816.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2002-594261/64.
XX
PT   Human activated Th1 and Th2 cell expression gene group, useful for the
PT   diagnosis and treatment of Th1 and Th2-related diseases.
XX
PS   Claim 1; Page 8; 60pp; Japanese.
XX
CC   The invention relates to SAGE (serial analysis of gene expression) tags
CC   representing groups of genes which are expressed in activated human Th1
CC   and/or Th2 cells. The SAGE tags of this invention consist of a sequence
CC   of 10 nucleotides located downstream of the 5'-CATG-3' sequence motif
CC   lying nearest to the polyA region of cDNAs derived from a variety of
CC   genes. These tags serve to uniquely identify each transcript and can thus
CC   be used to analyse the pattern of gene expression in particular cell
CC   types. The invention also relates to proteins encoded by the genes
CC   expressed in Th1 and/or Th2 cells, antibodies against these proteins, and
CC   inhibitors of the expression of groups of genes that are expressed in
CC   either or both the two cell types. Groups of genes expressed in Th1
CC   and/or Th2 cell types may be used for the diagnosis and treatment of Th1
CC   and Th2-related disorders. Sequences ABV78290-ABV78339 are SAGE tags
CC   representing 50 genes which are most highly expressed in Th1 cells
XX
SQ   Sequence 10 BP; 2 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TCTCCAGT 11
              ||||||||
Db          3 TCTCCAGT 10


RESULT 94
ABK23747
ID   ABK23747 standard; DNA; 10 BP.
```

```
XX
AC   ABK23747;
XX
DT   09-APR-2002  (first entry)
XX
DE   Transcript tag DNA sequence #336 induced or suppressed by N-myc.
XX
KW   Myc-dependent downstream gene; neoplastic; cancer; growth; invasion;
KW   spread; myc target; myc tag; SAGE; serial analysis of gene expression;
KW   myc oncogene; N-myc; human neuroblastoma; cytostatic; ds.
XX
OS   Homo sapiens.
XX
PN   WO200185941-A2.
XX
PD   15-NOV-2001.
XX
PF   11-MAY-2001; 2001WO-NL000361.
XX
PR   11-MAY-2000; 2000EP-00201698.
PR   29-JUN-2000; 2000EP-00202284.
XX
PA   (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.
XX
PI   Versteeg R,  Caron HN;
XX
DR   WPI; 2002-066603/09.
XX
PT   A new nucleic acid library of myc-dependent downstream genes capable of
PT   supporting a neoplastic characteristic of cancer is useful to find new
PT   therapies and diagnoses for cancer.
XX
PS   Disclosure; Page 58; 69pp; English.
XX
CC   The present invention relates to a nucleic acid library comprising myc-
CC   dependent downstream genes or their functional fragments essentially
CC   capable of supporting a neoplastic character of cancer such as growth,
CC   invasion or spread. These myc target or tag sequences are identified by
CC   SAGE (serial analysis of gene expression). The library is useful to find
CC   new diagnoses and treatments for cancer. The invention is also useful to
CC   enhance production of recombinant proteins in a production system with
CC   high expression of endogenous or transfected myc oncogenes. ABK23412-
CC   ABK23828 represent transcript tag DNA sequences that are activated or
CC   repressed by N-myc in human neuroblastoma
XX
SQ   Sequence 10 BP; 2 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TCTCCAGT 11
              ||||||||
Db          3 TCTCCAGT 10


RESULT 95
ABK23710
ID   ABK23710 standard; DNA; 10 BP.
XX
AC   ABK23710;
XX
DT   09-APR-2002  (first entry)
XX
DE   Transcript tag DNA sequence #299 induced or suppressed by N-myc.
XX
KW   Myc-dependent downstream gene; neoplastic; cancer; growth; invasion;
KW   spread; myc target; myc tag; SAGE; serial analysis of gene expression;
KW   myc oncogene; N-myc; human neuroblastoma; cytostatic; ds.
XX
OS   Homo sapiens.
XX
PN   WO200185941-A2.
XX
PD   15-NOV-2001.
XX
PF   11-MAY-2001; 2001WO-NL000361.
XX
PR   11-MAY-2000; 2000EP-00201698.
PR   29-JUN-2000; 2000EP-00202284.
XX
PA   (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.
XX
PI   Versteeg R,  Caron HN;
XX
DR   WPI; 2002-066603/09.
XX
PT   A new nucleic acid library of myc-dependent downstream genes capable of
PT   supporting a neoplastic characteristic of cancer is useful to find new
PT   therapies and diagnoses for cancer.
XX
PS   Disclosure; Page 57; 69pp; English.
XX
CC   The present invention relates to a nucleic acid library comprising myc-
CC   dependent downstream genes or their functional fragments essentially
CC   capable of supporting a neoplastic character of cancer such as growth,
CC   invasion or spread. These myc target or tag sequences are identified by
CC   SAGE (serial analysis of gene expression). The library is useful to find
CC   new diagnoses and treatments for cancer. The invention is also useful to
CC   enhance production of recombinant proteins in a production system with
CC   high expression of endogenous or transfected myc oncogenes. ABK23412-
CC   ABK23828 represent transcript tag DNA sequences that are activated or
CC   repressed by N-myc in human neuroblastoma
XX
SQ   Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CAGTCTCT 15
              ||||||||
Db          1 CAGTCTCT 8


RESULT 96
AAS97350
ID   AAS97350 standard; DNA; 10 BP.
XX
AC   AAS97350;
XX
DT   12-MAR-2002  (first entry)
XX
DE   Human CRYBB1 gene ASO primer extension PCR primer 3' end #9.
XX
KW   Human; crystallin beta B1; CRYBB1; chromosome 22q12.1; ophthalmalogical;
KW   cataract; allele specific oligonucleotide; ASO; ss; haplotype;
KW   genotyping; transgenic animal; PCR primer; primer extension.
XX
OS   Homo sapiens.
XX
PN   WO200185998-A1.
XX
PD   15-NOV-2001.
XX
PF   07-MAY-2001; 2001WO-US014715.
XX
PR   05-MAY-2000; 2000US-0202253P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Choi JY,  Kazemi A,  Kliem SE,  Koshy B,  Rounds E;
XX
DR   WPI; 2002-062253/08.
XX
PT   Novel polymorphic variants of crystallin, beta B1 useful in studying
```

PT expression and function of the protein, useful for screening candidate
PT drugs to treat diseases e.g. cataract.
XX
PS Claim 17; Page 13; 94pp; English.
XX
CC The invention relates to an isolated polynucleotide comprising a sequence
CC which is a polymorphic variant of a reference sequence for crystallin,
CC beta B1 (CRYBB1, located on chromosome 22q12.1) gene or their fragment,
CC where the polymorphic variant comprises a CRYBB1 isogene defined by a
CC haplotype from haplotypes 1-16 as given in the specification. Also
CC included are a transgenic non-human animal transformed or transfected
CC with the polymorphic variant, a computer system for storing and analysing
CC polymorphism data for CRYBB1 gene, a genome anthology for the CRYBB1 gene
CC which comprises the defined CRYBB1 isogenes, methods of determining an
CC individuals haplotype or genotype as well as methods of determining the
CC association of a particular haplotype with a disease or trait and a
CC composition comprising at least one genotyping oligonucleotide
CC (especially allele-specific oligonucleotides (ASO)) for detecting a
CC polymorphism in the CRYBB1. The isogenes or haplotypes are useful for
CC improving the efficiency and reliability of several steps in the
CC discovery and development of drugs for treating diseases associated with
CC CRYBB1 activity, e.g. cataract. and can also be used by the
CC pharmaceutical research scientist to validate CRYBB1 as a candidate
CC target for, and in design of clinical trials of candidate drugs for,
CC treating a specific condition drugs or disease predicted to be associated
CC with CRYBB1 activity. The ASOs are useful as probes and primers, and for
CC assaying a polymorphism in the target region. The present sequence is the
CC allele specific 3' end of a PCR primer used in primer extension
CC experiment to detect polymorphisms in CRYBB1
XX
SQ Sequence 10 BP; 0 A; 4 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGTCTCC 8
||||||||
Db 1 TTGTCTCC 8

RESULT 97
ACA94446
ID ACA94446 standard; DNA; 10 BP.
XX
AC ACA94446;
XX
DT 18-JUL-2003 (first entry)
XX
DE DNA tag from human transcript elevated in adenomas/cancers #27.
XX
KW Colorectal cancer; colorectal adenoma; ss; human; renal dipeptidase;
KW macrophage inhibitory cytokine; MIC; RDP; faeces; blood;
KW kidney proximal tubule.
XX
OS Homo sapiens.
XX
PN WO2003022863-A1.
XX
PD 20-MAR-2003.
XX
PF 09-SEP-2002; 2002WO-US028518.
XX
PR 07-SEP-2001; 2001US-0317494P.
PR 30-MAY-2002; 2002US-0383805P.
XX
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Buckhaults P, Kinzler KW, Vogelstein B;
XX
DR WPI; 2003-313220/30.
XX
PT Detecting colorectal cancer in a subject, involves detecting macrophage
PT inhibitory cytokine or renal dipeptidase or their mRNA in feces or blood
PT of the subject.
XX
PS Disclosure; Page 25; 59pp; English.
XX
CC The invention relates to detecting CC (colorectal cancer e.g. colorectal
CC adenoma), comprising: (a) detecting macrophage inhibitory cytokine (MIC)
CC or renal dipeptidase (RDP) in faeces or blood of a subject and comparing
CC amount of MIC or RDP detected to that in normal subjects, where an
CC elevated amount of MIC or RDP in the subject is an indicator of CC in
CC subject; (b) isolating mRNA sample from faeces of a subject, detecting
CC MIC or RDP mRNA in the mRNA sample, and comparing amount of MIC or RDP
CC mRNA detected to that in normal subjects, where an elevated amount of MIC
CC or RDP mRNA in the subject is an indicator of CC in subject; (c)
CC isolating epithelial cells from blood of a subject, isolating an mRNA
CC sample from faeces of a subject or epithelial cells, detecting MIC or RDP
CC mRNA in the mRNA sample, and comparing the amount of MIC or RDP mRNA in
CC the mRNA sample to amounts of MIC or RDP mRNA in normal subjects, where
CC an elevated amount of MIC or RDP mRNA in the mRNA sample is an indicative
CC of CC in the subject; (d) contacting blood or faeces of a subject, with
CC an RDP substrate, detecting activity of RDP in the blood or faeces by
CC detection of increased reaction product or decreased RDP substrate, and
CC comparing the amount of activity of RDP in blood or faeces of the subject
CC to that in normal subjects, where an elevated amount of activity of RDP
CC in the blood or faeces of the subject is an indicator of CC in the
CC subject; (e) administering to a subject an antibody which specifically
CC binds to RDP or an inhibitor of RDP, where the antibody or inhibitor is
CC labeled with a moiety which is detectable from outside of the subject and
CC detecting the moiety in the subject from outside of the subject, where an
CC area of localisation of the moiety within the subject but outside the
CC proximal tubules of the kidney identifies CC; or (f) administering to a
CC subject a substrate for RDP, the substrate being labeled with a
CC detectable moiety, isolating faeces or blood from the subject, and
CC detecting in the faeces or blood RDP reaction product or RDP substrate
CC with the detectable moiety, where increased product or decreased
CC substrate in the faeces or blood indicates CC in the subject. The methods
CC are useful for detecting colorectal cancer in a subject. The present
CC sequence is a DNA tag derived from a human transcript whose expression is
CC elevated in colorectal cancer or colorectal adenoma
XX
SQ Sequence 10 BP; 2 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCTCCAGT 11
||||||||
Db 3 TCTCCAGT 10

RESULT 98
ABT14242/c
ID ABT14242 standard; DNA; 10 BP.
XX
AC ABT14242;
XX
DT 20-FEB-2003 (first entry)
XX
DE Nucleic acid PCR amplification method-related RAPD PCR primer #12.
XX
KW Nucleic acid amplification; nucleic acid analysis; DNA analysis; ss;
KW RNA analysis; RAPD; PCR; primer; random amplified polymorphic DNA.
XX
OS Unidentified.
XX
PN WO200281743-A2.
XX
PD 17-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-GB001489.
XX
PR 02-APR-2001; 2001GB-00008182.

```
XX
PA   (HAMI/) HAMILL B.
XX
PI   Hamill B;
XX
DR   WPI; 2003-075484/07.
XX
PT   Amplification of nucleotide sequences from polynucleotides by chain
PT   extension of oligonucleotide primers, comprises 2 oligonucleotides in
PT   solution, 2 attached to supports and both share complementary sequences.
XX
PS   Disclosure; Fig 17; 60pp; English.
XX
CC   The invention comprises a method for the PCR amplification of nucleic
CC   acids. The method involves a set of primers, where two of the primers are
CC   in solution and at least two other primers are attached to a solid
CC   support. The method of the invention can be used for the analysis of a
CC   nucleic acid or a mixture of nucleic acids, including: single-stranded
CC   DNA molecules, double-stranded DNA molecules and mRNA molecules. The
CC   present DNA sequence represents a random amplified polymorphic DNA (RAPD)
CC   PCR primer of the invention
XX
SQ   Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CTCCAGTC 12
              ||||||||
Db          9 CTCCAGTC 2


RESULT 99
ADA00650
ID   ADA00650 standard; DNA; 10 BP.
XX
AC   ADA00650;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Oligonucleotide microchip associated probe #3.
XX
KW   discrete porous entity; microchip; cross contamination;
KW   chemical communication; co-polymerisation; ss; probe.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= Fluorescein"
XX
PN   US2003036063-A1.
XX
PD   20-FEB-2003.
XX
PF   15-AUG-2001; 2001US-00930865.
XX
PR   15-AUG-2001; 2001US-00930865.
XX
PA   (MIRZ/) MIRZABEKOV A.
PA   (TIMO/) TIMOFEEV E.
PA   (VASI/) VASILISKOV V.
XX
PI   Mirzabekov A,  Timofeev E,  Vasiliskov V;
XX
DR   WPI; 2003-605713/57.
XX
PT   Making discrete porous entities containing synthetic and natural
PT   compounds, useful as biochips, involves contacting each molecule at
PT   individual positions on insert substrate with compound, and solidifying
PT   the formed individual mixtures.
XX
PS   Example 2; Fig 5; 11pp; English.
XX
CC   The invention describes a method of making discrete porous entities that
CC   each contain a different molecule. The method comprises: positioning each
CC   different molecule at individual positions on an inert substrate;
CC   contacting each positioned molecule with compound to form individual
CC   mixtures; and solidifying the mixtures. The inventive method provides
CC   microchips that minimise any chance for cross contamination and chemical
CC   communication between entities. The contents of the entities do not mix
CC   with each other. It provides microchips having higher sensitivity and
CC   much faster kinetics of hybridisation. It facilitates the production of
CC   co-polymerised gel pads that can be as small as 3 x 3 microns. This
CC   sequence represents a associated with a oligonucleotide microchip
CC   prepared by photoinduced simultaneous co-polymerisation of 4 allyl-
CC   oligonucleotides.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 TCCAGTCT 13
              ||||||||
Db          2 TCCAGTCT 9


RESULT 100
ADL96158/c
ID   ADL96158 standard; DNA; 10 BP.
XX
AC   ADL96158;
XX
DT   20-MAY-2004  (first entry)
XX
DE   CD15+ myeloid cell associated probe seqid 56.
XX
KW   cytostatic; gene therapy; microarray; gene expression characteristic;
KW   haematopoietic cell; haematopoiesis; myeloid leukaemia; probe;
KW   CD15+ myeloid cell; ss.
XX
OS   Homo sapiens.
XX
PN   US2003165949-A1.
XX
PD   04-SEP-2003.
XX
PF   23-DEC-2002; 2002US-00329465.
XX
PR   27-DEC-2001; 2001US-0343826P.
XX
PA   (WANG/) WANG S M.
PA   (LEES/) LEE S.
PA   (CHEN/) CHEN J.
PA   (ZHOU/) ZHOU G.
PA   (ROWL/) ROWLEY J D.
XX
PI   Wang SM,  Lee S,  Chen J,  Zhou G,  Rowley JD;
XX
DR   WPI; 2003-863699/80.
XX
PT   New microarray for measuring gene expression characteristics of
PT   hematopoietic cells, useful for preparing a composition for diagnosing or
PT   treating myeloid leukemia.
XX
PS   Claim 1; SEQ ID NO 56; 32pp; English.
XX
CC   The invention describes a microarray for measuring gene expression
CC   characteristics of haematopoietic cells comprising at least 5
CC   polynucleotides having distinct sequences. Also described are: a method
CC   of diagnosing or treating an abnormality associated with haematopoiesis;
```

CC and diagnosing myeloid leukaemia in a patient. The microarray is useful
CC for preparing a composition for diagnosing or treating myeloid leukaemia.
CC This sequence represents a polynucleotide probe comprising a portion of
CC an expressed gene isolated from a population of CD15+ myeloid cells and
CC suitable for use in the microarray of the invention.
XX
SQ Sequence 10 BP; 4 A; 1 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCTCCAGT 11
||||||||
Db 10 TCTCCAGT 3

RESULT 101
ADI53195
ID ADI53195 standard; DNA; 10 BP.
XX
AC ADI53195;
XX
DT 22-APR-2004 (first entry)
XX
DE Human CD3E primer extension primer terminus #29.
XX
KW Human; CD3 antigen epsilon subunit; CD3E; primer; ss; haplotype;
KW genotype; primer extension.
XX
OS Homo sapiens.
XX
PN US2004018493-A1.
XX
PD 29-JAN-2004.
XX
PF 12-JUL-2002; 2002US-00193507.
XX
PR 12-JUL-2002; 2002US-00193507.
XX
PA (ANAS/) ANASTASIO A E.
PA (KAZE/) KAZEMI A.
PA (LACH/) LACHOWICZ M.
PA (PABO/) PABON V.
PA (SHAH/) SHAH N.
XX
PI Anastasio AE, Kazemi A, Lachowicz M, Pabon V, Shah N;
XX
DR WPI; 2004-122016/12.
XX
PT Haplotyping the CD3 antigen, epsilon subunit (CD3E) gene of an individual
PT by identifying the phased sequence of nucleotides at polymorphic sites
PT PS1-PS16 for at least one copy of the individual's CD3E gene.
XX
PS Claim 22; SEQ ID NO 80; 59pp; English.
XX
CC The invention relates to haplotyping the CD3 antigen, epsilon subunit
CC (CD3E) gene of an individual comprising identifying the phased sequence
CC of nucleotides at polymorphic sites PS1-PS16 for at least one copy of the
CC individual's CD3E gene and assigning to the individual a CD3E haplotype
CC or haplotype pair, given in the specification, that is consistent with
CC the phased sequence. Also included are genotyping the CD3E gene of an
CC individual, assigning a haplotype pair for the CD3E gene to an
CC individual, identifying an association between a trait and at least one
CC haplotype or haplotype pair of the CD3E gene, reducing the potential for
CC bias in a clinical trial of a candidate drug for treating a disease or
CC condition predicted to be associated with CD3E activity, an isolated CD3E
CC polynucleotide, a recombinant nonhuman organism transformed or
CC transfected with the isolated polynucleotide and expressing a CD3E
CC protein , an isolated fragment of a CD3E isogene (comprising at least 50
CC nucleotides in one of the regions of the CD3E gene (ADI53116) and one or
CC more polymorphisms (P1-P16), where the selected polymorphism has the
CC position given in the specification), screening for compounds targeting
CC the CD3E protein to treat a condition or disease predicted to be
CC associated with CD3E activity, validating the CD3E protein as a candidate
CC target for treating a medical condition predicted to be associated with
CC CD3E activity, an isolated oligonucleotide designed to detect a
CC polymorphism in the CD3E gene at polymorphic sites PS1-PS16, a kit for
CC haplotyping or genotyping the CD3E gene of an individual and a genome
CC anthology for the CD3 antigen, epsilon subunit (CD3E) gene which
CC comprises two or more CD3E isogenes. The method is useful for haplotyping
CC the CD3 antigen, epsilon subunit (CD3E) gene of an individual for
CC screening for compounds targeting the CD3E protein to treat a condition
CC or disease predicted to be associated with CD3E activity. The present
CC sequence is a Human CD3E primer extension primer terminus.
XX
SQ Sequence 10 BP; 1 A; 5 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCTCCAGT 11
||||||||
Db 3 TCTCCAGT 10

RESULT 102
ADK69774/c
ID ADK69774 standard; DNA; 10 BP.
XX
AC ADK69774;
XX
DT 06-MAY-2004 (first entry)
XX
DE Type 2 helper T (Th2) cell protein-related PCR primer SeqID5.
XX
KW Type 2 helper T cell; Th2 cell; Type 1 helper T cell; Th1 cell;
KW antiallergic; allergy; mouse; murine; ss; PCR; primer; ss.
XX
OS Mus musculus.
XX
PN JP2004016084-A.
XX
PD 22-JAN-2004.
XX
PF 14-JUN-2002; 2002JP-00175001.
XX
PR 14-JUN-2002; 2002JP-00175001.
XX
PA (MITU) MITSUBISHI CHEM CORP.
XX
DR WPI; 2004-113867/12.
XX
PT Novel protein expressing type 2 helper T cell, useful for controlling
PT immediate and delayed type allergy.
XX
PS Example 1; SEQ ID NO 5; 35pp; Japanese.
XX
CC This invention relates to a novel protein which is expressed in Type 2
CC helper T (Th2) cells, but not in Type 1 helper T (Th1) cells. The
CC invention may be useful for the production of compounds with an
CC antiallergic activity. The invention is useful for controlling immediate
CC and delayed type allergy. In addition, it may also be useful for
CC determining/analysing the risk of allergy developing in a subject. The
CC present sequence is that of a PCR primer which was used in the
CC exemplification of the invention.
XX
SQ Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CTCCAGTC 12
||||||||

```
Db          9 CTCCAGTC 2


RESULT 103
ADS77586
ID   ADS77586 standard; DNA; 10 BP.
XX
AC   ADS77586;
XX
DT   30-DEC-2004  (first entry)
XX
DE   Breast cancer detection oligonucleotide #1368.
XX
KW   ss; primer; cytostatic; RNA interference; RNAi; gene silencing;
KW   antisense oligonucleotide inhibitor; cathepsin K inhibitor;
KW   cathepsin L inhibitor; cathepsin F inhibitor;
KW   metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
KW   collagen antagonist; diagnosis; breast tissue; cancer.
XX
OS   Homo sapiens.
XX
PN   WO2004085621-A2.
XX
PD   07-OCT-2004.
XX
PF   22-MAR-2004; 2004WO-US008866.
XX
PR   20-MAR-2003; 2003US-0456735P.
XX
PA   (DAND ) DANA FARBER CANCER INST INC.
XX
PI   Polyak K,  Porter D,  Allinen M;
XX
DR   WPI; 2004-728732/71.
XX
PT   Diagnosing breast cancer comprises determining expression levels of a
PT   gene selected from those differentially expressed in normal or cancerous
PT   cells of a breast tissue sample including interleukin 1, thrombospondin 1
PT   and cystatin C.
XX
PS   Example 6; SEQ ID NO 1368; 149pp; English.
XX
CC   The invention relates to a method of diagnosis (M1) comprising: (a)
CC   providing a test sample of breast tissue; (b) determining the level of
CC   expression in the test sample of a gene (e.g. interleukin-8, superoxide
CC   dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
CC   specification, and (c) if the gene is expressed in the test sample at a
CC   lower level than in a control normal breast tissue sample, diagnosing the
CC   test sample as containing cancer cells. The method is used for diagnosing
CC   breast cancer. This sequence corresponds to an oligonucleotide primer
CC   used in the method of the invention.
XX
SQ   Sequence 10 BP; 2 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TCTCCAGT 11
              ||||||||
Db          3 TCTCCAGT 10


RESULT 104
ADS76686
ID   ADS76686 standard; DNA; 10 BP.
XX
AC   ADS76686;
XX
DT   30-DEC-2004  (first entry)
XX
DE   Breast cancer detection oligonucleotide #468.
XX
KW   ss; primer; cytostatic; RNA interference; RNAi; gene silencing;
KW   antisense oligonucleotide inhibitor; cathepsin K inhibitor;
KW   cathepsin L inhibitor; cathepsin F inhibitor;
KW   metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
KW   collagen antagonist; diagnosis; breast tissue; cancer.
XX
OS   Homo sapiens.
XX
PN   WO2004085621-A2.
XX
PD   07-OCT-2004.
XX
PF   22-MAR-2004; 2004WO-US008866.
XX
PR   20-MAR-2003; 2003US-0456735P.
XX
PA   (DAND ) DANA FARBER CANCER INST INC.
XX
PI   Polyak K,  Porter D,  Allinen M;
XX
DR   WPI; 2004-728732/71.
XX
PT   Diagnosing breast cancer comprises determining expression levels of a
PT   gene selected from those differentially expressed in normal or cancerous
PT   cells of a breast tissue sample including interleukin 1, thrombospondin 1
PT   and cystatin C.
XX
PS   Example 2; SEQ ID NO 468; 149pp; English.
XX
CC   The invention relates to a method of diagnosis (M1) comprising: (a)
CC   providing a test sample of breast tissue; (b) determining the level of
CC   expression in the test sample of a gene (e.g. interleukin-8, superoxide
CC   dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
CC   specification, and (c) if the gene is expressed in the test sample at a
CC   lower level than in a control normal breast tissue sample, diagnosing the
CC   test sample as containing cancer cells. The method is used for diagnosing
CC   breast cancer. This sequence corresponds to an oligonucleotide primer
CC   used in the method of the invention.
XX
SQ   Sequence 10 BP; 2 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TCTCCAGT 11
              ||||||||
Db          3 TCTCCAGT 10


RESULT 105
ADS77754
ID   ADS77754 standard; DNA; 10 BP.
XX
AC   ADS77754;
XX
DT   30-DEC-2004  (first entry)
XX
DE   Breast cancer detection oligonucleotide #1536.
XX
KW   ss; primer; cytostatic; RNA interference; RNAi; gene silencing;
KW   antisense oligonucleotide inhibitor; cathepsin K inhibitor;
KW   cathepsin L inhibitor; cathepsin F inhibitor;
KW   metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
KW   collagen antagonist; diagnosis; breast tissue; cancer.
XX
OS   Homo sapiens.
XX
PN   WO2004085621-A2.
XX
PD   07-OCT-2004.
XX
PF   22-MAR-2004; 2004WO-US008866.
```

XX
PR 20-MAR-2003; 2003US-0456735P.
XX
PA (DAND) DANA FARBER CANCER INST INC.
XX
PI Polyak K, Porter D, Allinen M;
XX
DR WPI; 2004-728732/71.
XX
PT Diagnosing breast cancer comprises determining expression levels of a
PT gene selected from those differentially expressed in normal or cancerous
PT cells of a breast tissue sample including interleukin 1, thrombospondin 1
PT and cystatin C.
XX
PS Example 6; SEQ ID NO 1536; 149pp; English.
XX
CC The invention relates to a method of diagnosis (M1) comprising: (a)
CC providing a test sample of breast tissue; (b) determining the level of
CC expression in the test sample of a gene (e.g. interleukin-8, superoxide
CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
CC specification, and (c) if the gene is expressed in the test sample at a
CC lower level than in a control normal breast tissue sample, diagnosing the
CC test sample as containing cancer cells. The method is used for diagnosing
CC breast cancer. This sequence corresponds to an oligonucleotide primer
CC used in the method of the invention.
XX
SQ Sequence 10 BP; 2 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCTCCAGT 11
||||||||
Db 3 TCTCCAGT 10

RESULT 106
ADZ85566
ID ADZ85566 standard; DNA; 10 BP.
XX
AC ADZ85566;
XX
DT 28-JUL-2005 (first entry)
XX
DE Human BACE455 cDNA PCR primer #7.
XX
KW Beta-secretase 455; beta-secretase; BACE455; neurodegenerative disease;
KW Alzheimers disease; Down syndrome; glaucoma; Parkinsons disease;
KW motor neurone disease; cerebrovascular ischemia; dementia;
KW neuroprotective; nootropic; ophthalmological; antiparkinsonian;
KW cerebroprotective; vasotropic; CNS-Gen.; muscular-gen.; PCR; ss; primer.
XX
OS Homo sapiens.
XX
PN WO2005045021-A1.
XX
PD 19-MAY-2005.
XX
PF 05-NOV-2004; 2004WO-IB003897.
XX
PR 06-NOV-2003; 2003US-0517401P.
XX
PA (EXON-) EXONHIT THERAPEUTICS SA.
XX
PI Desire L;
XX
DR WPI; 2005-366843/37.
XX
PT New beta-secretase 455 polypeptide, useful for detecting presence of
PT neurodegenerative disease or associated disorder, for assessing response
PT of subject to treatment of neuro-degenerative disease or associated
PT disorder.
XX
PS Disclosure; SEQ ID NO 21; 77pp; English.
XX
CC The invention relates to a human beta-secretase (BACE) 455 polypeptide or
CC a distinctive fragment of the polypeptide. The invention also relates to
CC an isolated polynucleotide encoding the polypeptide, a vector comprising
CC the polynucleotide, an inhibitory nucleic acid molecule that hybridizes
CC under physiological conditions to a nucleic acid molecule encoding a
CC BACE455 polypeptide and selectively inhibits its transcription or
CC translation, a BACE455 inhibitor that inhibits the expression or activity
CC of a BACE455 polypeptide or polynucleotide, a pharmaceutical composition
CC comprising a BACE455 inhibitor and a carrier or vehicle, a method of
CC selecting, characterizing, screening or optimizing a biologically active
CC compound involving contacting a test compound with a BACE455
CC polynucleotide, polypeptide or distinctive fragment of the polynucleotide
CC or polypeptide and determining whether the test compound binds the
CC BACE455 polynucleotide or polypeptide or modulates an activity of the
CC BACE455 polynucleotide or polypeptide, a method of detecting the presence
CC of or predisposition to a neurodegenerative disease or an associated
CC disorder in a subject involving detecting the presence of a BACE455
CC polynucleotide or polypeptide in a sample from the subject, a method of
CC assessing the response of a subject to a treatment of a neurodegenerative
CC disease or an associated disorder involving detecting the presence of a
CC BACE455 polynucleotide or polypeptide in a sample from the subject, a
CC method of determining the efficacy of a treatment of a neurodegenerative
CC disease or an associated disorder in a subject involving determining the
CC presence and/or abundance of a BACE455 polynucleotide or polypeptide in a
CC sample taken from the subject during or after the treatment and comparing
CC the presence and/or abundance to a reference sample from the subject
CC prior to or at an earlier stage of the treatment, a method of producing
CC an antibody that binds a BACE455 polypeptide, and a method of producing a
CC composition comprising a BACE455 inhibitor. The sequences, methods and
CC compositions of the invention are useful for treating or preventing a
CC neurodegenerative disease or an associated disorder in a subject, such as
CC Alzheimers disease, Down syndrome, glaucoma, Parkinsons disease,
CC amyotrophic lateral sclerosis, stroke and dementia. This sequence
CC represents a PCR primer used to amplify cDNA encoding the human BACE455
CC polypeptide of the invention.
XX
SQ Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CAGTCTCT 15
||||||||
Db 1 CAGTCTCT 8

RESULT 107
AAZ86307
ID AAZ86307 standard; DNA; 10 BP.
XX
AC AAZ86307;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #5541.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.

PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 205; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effecter
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 26.0%; Score 5.2; DB 1; Length 10;
Best Local Similarity 70.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CTCCAGTCTC 14
|| || |||
Db 1 CTGGAGACTC 10

RESULT 108
AAZ81791/c
ID AAZ81791 standard; DNA; 10 BP.
XX
AC AAZ81791;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #1025.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 86; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effecter
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 3 A; 4 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 26.0%; Score 5.2; DB 1; Length 10;
Best Local Similarity 70.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TGTCTCCAGT 11
|| || |||
Db 10 TGACTGGAGT 1

RESULT 109
AAF39425
ID AAF39425 standard; DNA; 10 BP.
XX
AC AAF39425;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6164.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX

PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 220; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 4 A; 3 C; 2 G; 1 T; 0 U; 0 Other;

```
  Query Match             24.0%;  Score 4.8;  DB 1;  Length 10;
  Best Local Similarity   75.0%;  Pred. No. 1.1e+02;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CTCCAGTC 12
              || ||| |
Db          2 CTGCAGAC 9
```

RESULT 110
ADQ32655
ID ADQ32655 standard; DNA; 11 BP.
XX
AC ADQ32655;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human facial skin-associated DNA fragment SEQ ID NO 745.
XX
KW facial skin; human; serial analysis of gene expression; SAGE;
KW homeostasis; biochip; cosmetic; pharmaceutical; ds.
XX
OS Homo sapiens.
XX
PN DE10260928-A1.
XX
PD 08-JUL-2004.
XX
PF 20-DEC-2002; 2002DE-01060928.
XX
PR 20-DEC-2002; 2002DE-01060928.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
PI Conradt M, Hofmann K;
XX
DR WPI; 2004-518855/50.
XX
PT In vitro identification of genes important for facial skin, useful for
PT assessing homeostasis and in screening for pharmaceutical or cosmetic
PT agents, based on differential expression analysis.
XX
PS Claim 5; SEQ ID NO 745; 577pp; German.
XX
CC This invention describes a novel in vitro method for identifying genes
CC that are significant for facial skin in humans. The method comprises
CC recovering, from facial skin, a first mixture of genetically expressed
CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or
CC their fragments), recovering a second, similar mixture from some other
CC human tissue, preferably skin from a protected area, especially from the
CC breast and subjecting the mixtures to serial analysis of gene expression
CC (SAGE) to identify those genes for which expression is markedly different
CC between facial skin and the other tissue. The invention also describes an
CC in vitro method for determining homeostasis of human facial skin; a test
CC kit which comprises a solid support (flexible or rigid) on which are
CC immobilised probes that bind specifically to the factors of interest and
CC a biochip for determining homeostasis of human facial skin. The products
CC of the invention are also used in a method which determines activity of
CC cosmetic and pharmaceutical agents for use against disorders or
CC disturbances of the homeostasis of human skin and a screening method for
CC identifying cosmetic and pharmaceutical agents. The method allows
CC identification of as many as possible of the genes important for facial
CC skin and thus of a very wide range of potential therapeutic and cosmetic
CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to
CC identify the facial skin-associated genes described in the invention.
XX
SQ Sequence 11 BP; 5 A; 3 C; 2 G; 1 T; 0 U; 0 Other;

```
  Query Match             24.0%;  Score 4.8;  DB 1;  Length 11;
  Best Local Similarity   75.0%;  Pred. No. 1.2e+02;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CTCCAGTC 12
              || ||| |
Db          2 CTGCAGAC 9
```

RESULT 111
AAF42075/c
ID AAF42075 standard; DNA; 10 BP.
XX
AC AAF42075;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8814.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.

XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 314; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 1 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 22.0%; Score 4.4; DB 1; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 AGTCTC 14
|| |||
Db 6 AGACTC 1

RESULT 112
AAZ81566/c
ID AAZ81566 standard; DNA; 10 BP.
XX
AC AAZ81566;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #800.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 79; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effecter
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 2 A; 3 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 22.0%; Score 4.4; DB 1; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CAGTCT 13
||| ||
Db 10 CAGACT 5

RESULT 113
AAQ88288/c
ID AAQ88288 standard; DNA; 10 BP.
XX
AC AAQ88288;
XX
DT 27-AUG-2003 (revised)
DT 12-DEC-1995 (first entry)
XX
DE 5'-target sequence 2 for detection of fruit species by PCR.
XX
KW Polymerase chain reaction amplification; fruit juice; fruit pulp;
KW species detection; apple; orange; grapefruit; RAPD technique; ss.
XX
OS Citrus.

XX
PN FR2711143-A1.
XX
PD 21-APR-1995.
XX
PF 13-OCT-1994; 94FR-00012235.
XX
PR 13-OCT-1993; 93GB-00021113.
XX
PA (UKAG-) UK MIN AGRIC FISHERIES & FOOD.
XX
PI Lindsey K, Twell D;
XX
DR WPI; 1995-157154/21.
XX
PT Identifying species, variety etc. of fruits by PCR amplification - then
PT comparing products with standards, also new test kits, primers and
PT hybridisation probes, partic. to detect fraudulent use in food prodn.
XX
PS Claim 7; Page 17; 20pp; French.
XX
CC Primers have been identified which give useful results for identification
CC of genus, species or variety of fruits (see AAQ88293-Q88298);
CC amplification profiles are established using several of the primers,
CC which are complementary to regions (see AAQ88287-Q88292) at the 5'-end of
CC the target sequences which are amplified. Using the primers it was
CC possible to distinguish between e.g. different varieties of Navel oranges
CC and also between "red" apples and "Granny Smith" apples. (Updated on 27-
CC AUG-2003 to correct OS field.)
XX
SQ Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 21.0%; Score 4.2; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GTCTCCAGT 11
| || |||
Db 9 GACTGGAGT 1

RESULT 114
AAQ88294
ID AAQ88294 standard; DNA; 10 BP.
XX
AC AAQ88294;
XX
DT 12-DEC-1995 (first entry)
XX
DE Primer sequence 8 for detection of fruit species by PCR.
XX
KW Polymerase chain reaction amplification; fruit juice; fruit pulp;
KW species detection; apple; orange; grapefruit; RAPD technique; ss.
XX
OS Synthetic.
XX
PN FR2711143-A1.
XX
PD 21-APR-1995.
XX
PF 13-OCT-1994; 94FR-00012235.
XX
PR 13-OCT-1993; 93GB-00021113.
XX
PA (UKAG-) UK MIN AGRIC FISHERIES & FOOD.
XX
PI Lindsey K, Twell D;
XX
DR WPI; 1995-157154/21.
XX
PT Identifying species, variety etc. of fruits by PCR amplification - then
PT comparing products with standards, also new test kits, primers and
PT hybridisation probes, partic. to detect fraudulent use in food prodn.
XX
PS Claim 8; Page 17; 20pp; French.
XX
CC Primers have been identified which give useful results for identification
CC of genus, species or variety of fruits (see AAQ88293-Q88298);
CC amplification profiles are established using several of the primers,
CC which are complementary to regions (see AAQ88287-Q88292) at the 5'-end of
CC the target sequences which are amplified. Using the primers it was
CC possible to distinguish between e.g. different varieties of Navel oranges
CC and also between "red" apples and "Granny Smith" apples
XX
SQ Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 21.0%; Score 4.2; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GTCTCCAGT 11
| || |||
Db 2 GACTGGAGT 10

RESULT 115
AAZ08343
ID AAZ08343 standard; DNA; 10 BP.
XX
AC AAZ08343;
XX
DT 13-OCT-1999 (first entry)
XX
DE Nilaparvata lugens Stal. rice PCR primer sequence #9.
XX
KW Nilaparvata lugens Stal; rice; detection; resistance; PCR marker; bph-2;
KW PCR primer; ss.
XX
OS Synthetic.
OS Nilaparvata lugens.
XX
PN JP11206376-A.
XX
PD 03-AUG-1999.
XX
PF 22-JAN-1998; 98JP-00010845.
XX
PR 22-JAN-1998; 98JP-00010845.
XX
PA (AICH-) AICHI KEN PREFECTURE.
XX
DR WPI; 1999-486354/41.
XX
PT Detection of resistance to Nilaparvata lugens Stal. rice - using
PT amplification techniques.
XX
PS Example; Page 11; 15pp; Japanese.
XX
CC A method has been developed for the detection of resistance to
CC Nilaparvata lugens Stal. rice. The method comprises: (1) amplification of
CC a DNA fragment by PCR using a PCR marker and detection of the resistance,
CC in which a DNA fragment being specifically amplified in a species having
CC a gene (bph-2) resistant to Nilaparvata lugens Stal. using a genome DNA
CC of rice as a template and 1.3 Kbp in total with a base sequence shown by
CC sequence 1 (AAZ08335), comprising 300 bases at 5'-terminal and sequence 2
CC (AAZ08336) comprising 290 bases at 3'-terminal, respectively; and (2) a
CC PCR marker comprising a sense primer of base numbers shown in sequence 3
CC (AAZ08337) and an antisense primer of base numbers shown in sequence 5
CC (AAZ08341). The present invention also describes a primer for PCR using
CC rice genome of sequences 9, 10 or 11 (AAZ08343 to AAZ08345), or a couple
CC of sense primer of sequences 3 or 7 (AAZ08341), respectively, for
CC detection of the resistance. The method is used for the simple detection
CC of resistance to Nilaparvata lugens Stal
XX
SQ Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

```
  Query Match             21.0%;  Score 4.2;  DB 1;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 1.3e+02;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 TCTCCAGTC 12
              |||  || |
Db          2 TCTGGAGAC 10


RESULT 116
AAA70756
ID   AAA70756 standard; DNA; 10 BP.
XX
AC   AAA70756;
XX
DT   17-JAN-2001  (first entry)
XX
DE   PCR primer #2 for B. pumilus strain B3 DNA amplification.
XX
KW   PCR primer; amplification; Bacillus pumilus B3; CECT 5105; plant growth;
KW   Bacillus licheniformis B12; CECT 5106; gibberellin; plant hormone;
KW   woody plant; herbaceous plant; disease resistance; ss.
XX
OS   Bacillus pumilus.
XX
PN   WO200043497-A1.
XX
PD   27-JUL-2000.
XX
PF   18-JAN-2000; 2000WO-ES000017.
XX
PR   20-JAN-1999;   99ES-00000106.
XX
PA   (UYSA-) UNIV SAN PABLO CEU.
XX
PI   Gutierrez Manero J,  Probanza Lobo A;
XX
DR   WPI; 2000-499226/44.
XX
PT   New strains of Bacillus, useful for promoting growth of herbaceous and
PT   woody plants, produce gibberellin plant hormones.
XX
PS   Disclosure; Page 15; 28pp; Spanish.
XX
CC   The invention relates to the isolation of novel strains of bacteria
CC   (Bacillus pumilus B3 (CECT 5105) and B. licheniformis B12 (CECT 5106))
CC   which produce gibberellin plant hormones that regulate plant growth. The
CC   plant growth hormones are produced at level of 0.0029-0.148 mg/l by B3
CC   and at 0.0017-0.123 mg/l by B12, after 24 hour culture at 28 deg. C in
CC   liquid medium. The new strains are used to treat cultured plants (both
CC   woody and herbaceous) to increase their growth, vigour and disease
CC   resistance. Primers AAA70755-A70762 were used to PCR amplify DNA from the
CC   B. pumilus strain B3
XX
SQ   Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             21.0%;  Score 4.2;  DB 1;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 1.3e+02;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAGT 11
              | ||  |||
Db          2 GACTGGAGT 10


RESULT 117
AAH41695
ID   AAH41695 standard; DNA; 10 BP.
XX
AC   AAH41695;
XX
DT   28-AUG-2001  (first entry)
XX
DE   Anti-PEP gene construction related oligonucleotide S4.
XX
KW   Phosphoenopyruvate carboxylase; PEPCase; seed; acetyl-CoA carboxylase;
KW   oilseed; PEP; plant breeding; soya bean; sunflower; rapeseed; peanut;
KW   sesame; crop plant; protein content; fatty acid content; anti-PEP; ss.
XX
OS   Synthetic.
XX
PN   WO200134812-A1.
XX
PD   17-MAY-2001.
XX
PF   06-NOV-2000; 2000WO-CN000418.
XX
PR   09-NOV-1999;   99CN-00124511.
XX
PA   (ZHEJ-) ZHEJIANG AGRIC SCI ACAD.
XX
PI   Chen J,  Lang C,  Huang R,  Hu Z,  Liu Z;
XX
DR   WPI; 2001-335934/35.
XX
PT   Altering protein/fatty acid composition of seeds, useful for producing
PT   e.g. soya bean or sesame seed with high protein/fatty acid content,
PT   comprises introducing antisense gene.
XX
PS   Example 8; Page 8; 25pp; Chinese.
XX
CC   The present invention describes a method for altering the protein/fatty
CC   acid composition of seeds. The method comprises: (1) cloning
CC   phosphoenopyruvate carboxylase (PEP) or acetyl-CoA carboxylase (ACC)
CC   genes or their fragments; (2) constructing the corresponding antisense
CC   gene of anti-PEP or anti-ACC; and (3) introducing the antisense gene into
CC   the plant cell of a crop. The method is applicable in plant breeding to
CC   give oilseed crops with high oil or protein content like soya bean,
CC   sunflower, rapeseed, peanut and sesame. The produced crop plants have
CC   high yield of oil or protein. The present sequence represents an
CC   oligonucleotide which is used in the construction of an anti-PEP gene in
CC   an example from the present invention
XX
SQ   Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             21.0%;  Score 4.2;  DB 1;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 1.3e+02;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAGT 11
              | ||  |||
Db          2 GACTGGAGT 10


RESULT 118
ABT14242
ID   ABT14242 standard; DNA; 10 BP.
XX
AC   ABT14242;
XX
DT   20-FEB-2003  (first entry)
XX
DE   Nucleic acid PCR amplification method-related RAPD PCR primer #12.
XX
KW   Nucleic acid amplification; nucleic acid analysis; DNA analysis; ss;
KW   RNA analysis; RAPD; PCR; primer; random amplified polymorphic DNA.
XX
OS   Unidentified.
XX
PN   WO200281743-A2.
XX
PD   17-OCT-2002.
XX
PF   28-MAR-2002; 2002WO-GB001489.
XX
PR   02-APR-2001; 2001GB-00008182.
```

XX
PA (HAMI/) HAMILL B.
XX
PI Hamill B;
XX
DR WPI; 2003-075484/07.
XX
PT Amplification of nucleotide sequences from polynucleotides by chain
PT extension of oligonucleotide primers, comprises 2 oligonucleotides in
PT solution, 2 attached to supports and both share complementary sequences.
XX
PS Disclosure; Fig 17; 60pp; English.
XX
CC The invention comprises a method for the PCR amplification of nucleic
CC acids. The method involves a set of primers, where two of the primers are
CC in solution and at least two other primers are attached to a solid
CC support. The method of the invention can be used for the analysis of a
CC nucleic acid or a mixture of nucleic acids, including: single-stranded
CC DNA molecules, double-stranded DNA molecules and mRNA molecules. The
CC present DNA sequence represents a random amplified polymorphic DNA (RAPD)
CC PCR primer of the invention
XX
SQ Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 21.0%; Score 4.2; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GTCTCCAGT 11
| || |||
Db 2 GACTGGAGT 10

RESULT 119
ADK69774
ID ADK69774 standard; DNA; 10 BP.
XX
AC ADK69774;
XX
DT 06-MAY-2004 (first entry)
XX
DE Type 2 helper T (Th2) cell protein-related PCR primer SeqID5.
XX
KW Type 2 helper T cell; Th2 cell; Type 1 helper T cell; Th1 cell;
KW antiallergic; allergy; mouse; murine; ss; PCR; primer; ss.
XX
OS Mus musculus.
XX
PN JP2004016084-A.
XX
PD 22-JAN-2004.
XX
PF 14-JUN-2002; 2002JP-00175001.
XX
PR 14-JUN-2002; 2002JP-00175001.
XX
PA (MITU) MITSUBISHI CHEM CORP.
XX
DR WPI; 2004-113867/12.
XX
PT Novel protein expressing type 2 helper T cell, useful for controlling
PT immediate and delayed type allergy.
XX
PS Example 1; SEQ ID NO 5; 35pp; Japanese.
XX
CC This invention relates to a novel protein which is expressed in Type 2
CC helper T (Th2) cells, but not in Type 1 helper T (Th1) cells. The
CC invention may be useful for the production of compounds with an
CC antiallergic activity. The invention is useful for controlling immediate
CC and delayed type allergy. In addition, it may also be useful for
CC determining/analysing the risk of allergy developing in a subject. The
CC present sequence is that of a PCR primer which was used in the
CC exemplification of the invention.
XX
SQ Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 21.0%; Score 4.2; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GTCTCCAGT 11
| || |||
Db 2 GACTGGAGT 10

RESULT 120
ADZ85566/c
ID ADZ85566 standard; DNA; 10 BP.
XX
AC ADZ85566;
XX
DT 28-JUL-2005 (first entry)
XX
DE Human BACE455 cDNA PCR primer #7.
XX
KW Beta-secretase 455; beta-secretase; BACE455; neurodegenerative disease;
KW Alzheimers disease; Down syndrome; glaucoma; Parkinsons disease;
KW motor neurone disease; cerebrovascular ischemia; dementia;
KW neuroprotective; nootropic; ophthalmological; antiparkinsonian;
KW cerebroprotective; vasotropic; CNS-Gen.; muscular-gen.; PCR; ss; primer.
XX
OS Homo sapiens.
XX
PN WO2005045021-A1.
XX
PD 19-MAY-2005.
XX
PF 05-NOV-2004; 2004WO-IB003897.
XX
PR 06-NOV-2003; 2003US-0517401P.
XX
PA (EXON-) EXONHIT THERAPEUTICS SA.
XX
PI Desire L;
XX
DR WPI; 2005-366843/37.
XX
PT New beta-secretase 455 polypeptide, useful for detecting presence of
PT neurodegenerative disease or associated disorder, for assessing response
PT of subject to treatment of neuro-degenerative disease or associated
PT disorder.
XX
PS Disclosure; SEQ ID NO 21; 77pp; English.
XX
CC The invention relates to a human beta-secretase (BACE) 455 polypeptide or
CC a distinctive fragment of the polypeptide. The invention also relates to
CC an isolated polynucleotide encoding the polypeptide, a vector comprising
CC the polynucleotide, an inhibitory nucleic acid molecule that hybridizes
CC under physiological conditions to a nucleic acid molecule encoding a
CC BACE455 polypeptide and selectively inhibits its transcription or
CC translation, a BACE455 inhibitor that inhibits the expression or activity
CC of a BACE455 polypeptide or polynucleotide, a pharmaceutical composition
CC comprising a BACE455 inhibitor and a carrier or vehicle, a method of
CC selecting, characterizing, screening or optimizing a biologically active
CC compound involving contacting a test compound with a BACE455
CC polynucleotide, polypeptide or distinctive fragment of the polynucleotide
CC or polypeptide and determining whether the test compound binds the
CC BACE455 polynucleotide or polypeptide or modulates an activity of the
CC BACE455 polynucleotide or polypeptide, a method of detecting the presence
CC of or predisposition to a neurodegenerative disease or an associated
CC disorder in a subject involving detecting the presence of a BACE455
CC polynucleotide or polypeptide in a sample from the subject, a method of
CC assessing the response of a subject to a treatment of a neurodegenerative
CC disease or an associated disorder involving detecting the presence of a
CC BACE455 polynucleotide or polypeptide in a sample from the subject, a
CC method of determining the efficacy of a treatment of a neurodegenerative

```
CC   disease or an associated disorder in a subject involving determining the
CC   presence and/or abundance of a BACE455 polynucleotide or polypeptide in a
CC   sample taken from the subject during or after the treatment and comparing
CC   the presence and/or abundance to a reference sample from the subject
CC   prior to or at an earlier stage of the treatment, a method of producing
CC   an antibody that binds a BACE455 polypeptide, and a method of producing a
CC   composition comprising a BACE455 inhibitor. The sequences, methods and
CC   compositions of the invention are useful for treating or preventing a
CC   neurodegenerative disease or an associated disorder in a subject, such as
CC   Alzheimers disease, Down syndrome, glaucoma, Parkinsons disease,
CC   amyotrophic lateral sclerosis, stroke and dementia. This sequence
CC   represents a PCR primer used to amplify cDNA encoding the human BACE455
CC   polypeptide of the invention.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             21.0%;  Score 4.2;  DB 1;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 1.3e+02;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          7 CCAGTCTCT 15
              ||||   ||
Db         10 CCAGAGACT 2


RESULT 121
ADR36038
ID   ADR36038 standard; DNA; 9 BP.
XX
AC   ADR36038;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Human nicking agent DNA containing BstNBI restriction site #2458.
XX
KW   ss; nicking agent; assay panel; diagnosis; expression pattern;
KW   DNA fingerprinting; nosocomial infection; microbiological assay;
KW   bacterial contamination; genome mapping; bioremediation.
XX
OS   Homo sapiens.
XX
PN   WO2004067765-A2.
XX
PD   12-AUG-2004.
XX
PF   29-JAN-2004; 2004WO-US002720.
XX
PR   29-JAN-2003; 2003US-0443811P.
XX
PA   (KECK-) KECK GRADUATE INST.
XX
PI   Van Ness J,  Galas DJ,  Van Ness LK;
XX
DR   WPI; 2004-581010/56.
XX
PT   Identifying nucleic acid sample source, useful for identifying bacterial
PT   strains involved in nosocomial infections, comprises treating the nucleic
PT   acid sample with components comprising a nicking agent under nicking
PT   conditions.
XX
PS   Example 3; Page 105-219; 238pp; English.
XX
CC   The invention relates to a method of treating a nucleic acid sample with
CC   components under nicking conditions, where the components comprise a
CC   nicking agent, and the conditions cause the nicking agent to nick the
CC   nucleic acid sample to thus produce a family of initiating
CC   oligonucleotide fragments, and subjecting one or more members of the
CC   family of initiating oligonucleotide fragments to a characterization
CC   process to thus provide results. The method is useful for creating an
CC   assay panel of diagnostic oligonucleotides that can identify any organism
CC   or individual. The method is useful for characterizing other DNA
CC   molecules e.g., cDNA, and for characterizing cDNA expression patterns.
CC   The method, kit or composition is useful for identifying the source
CC   organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC   non-human animal or human. The method is particularly useful for rapidly
CC   fingerprinting DNA to identifying prokaryotic and eukaryotic species,
CC   subspecies, and especially strains or individuals of the subspecies. It
CC   is especially useful for identifying different bacterial strains involved
CC   in e.g., nosocomial infections. Furthermore, the method is useful for
CC   diagnosing bacterial disease in plants and humans, monitoring for
CC   bacterial content and/or contamination in the environment, monitoring
CC   food for bacterial contamination, monitoring manufacturing processes for
CC   bacterial contamination, monitoring quality assurance/quality control of
CC   laboratory tests involving microbiological assays, tracing bacterial
CC   contamination and/or outbreaks of bacterial infections, genome mapping,
CC   monitoring bioremediation sites, and for monitoring agricultural sites
CC   for test crops, bacteria and recombinant molecules. Sequences ADR33581-
CC   ADR37496 correspond to target nucleic acids containing an NBstNBI
CC   restriction site and used in the method of the invention.
XX
SQ   Sequence 9 BP; 4 A; 1 C; 2 G; 1 T; 0 U; 1 Other;

  Query Match             20.0%;  Score 4;  DB 1;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 2.5e+02;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 CAGTCT 13
              :|| ||
Db          3 SAGACT 8


RESULT 122
ADR36039
ID   ADR36039 standard; DNA; 9 BP.
XX
AC   ADR36039;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Human nicking agent DNA containing BstNBI restriction site #2459.
XX
KW   ss; nicking agent; assay panel; diagnosis; expression pattern;
KW   DNA fingerprinting; nosocomial infection; microbiological assay;
KW   bacterial contamination; genome mapping; bioremediation.
XX
OS   Homo sapiens.
XX
PN   WO2004067765-A2.
XX
PD   12-AUG-2004.
XX
PF   29-JAN-2004; 2004WO-US002720.
XX
PR   29-JAN-2003; 2003US-0443811P.
XX
PA   (KECK-) KECK GRADUATE INST.
XX
PI   Van Ness J,  Galas DJ,  Van Ness LK;
XX
DR   WPI; 2004-581010/56.
XX
PT   Identifying nucleic acid sample source, useful for identifying bacterial
PT   strains involved in nosocomial infections, comprises treating the nucleic
PT   acid sample with components comprising a nicking agent under nicking
PT   conditions.
XX
PS   Example 3; Page 105-219; 238pp; English.
XX
CC   The invention relates to a method of treating a nucleic acid sample with
CC   components under nicking conditions, where the components comprise a
CC   nicking agent, and the conditions cause the nicking agent to nick the
CC   nucleic acid sample to thus produce a family of initiating
CC   oligonucleotide fragments, and subjecting one or more members of the
CC   family of initiating oligonucleotide fragments to a characterization
CC   process to thus provide results. The method is useful for creating an
CC   assay panel of diagnostic oligonucleotides that can identify any organism
```

```
CC   or individual. The method is useful for characterizing other DNA
CC   molecules e.g., cDNA, and for characterizing cDNA expression patterns.
CC   The method, kit or composition is useful for identifying the source
CC   organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC   non-human animal or human. The method is particularly useful for rapidly
CC   fingerprinting DNA to identifying prokaryotic and eukaryotic species,
CC   subspecies, and especially strains or individuals of the subspecies. It
CC   is especially useful for identifying different bacterial strains involved
CC   in e.g., nosocomial infections. Furthermore, the method is useful for
CC   diagnosing bacterial disease in plants and humans, monitoring for
CC   bacterial content and/or contamination in the environment, monitoring
CC   food for bacterial contamination, monitoring manufacturing processes for
CC   bacterial contamination, monitoring quality assurance/quality control of
CC   laboratory tests involving microbiological assays, tracing bacterial
CC   contamination and/or outbreaks of bacterial infections, genome mapping,
CC   monitoring bioremediation sites, and for monitoring agricultural sites
CC   for test crops, bacteria and recombinant molecules. Sequences ADR33581-
CC   ADR37496 correspond to target nucleic acids containing an NBstNBI
CC   restriction site and used in the method of the invention.
XX
SQ   Sequence 9 BP; 4 A; 1 C; 2 G; 1 T; 0 U; 1 Other;

  Query Match             20.0%;  Score 4;  DB 1;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 2.5e+02;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 CAGTCT 13
              :|| ||
Db          3 SAGACT 8


RESULT 123
ADR36041
ID   ADR36041 standard; DNA; 9 BP.
XX
AC   ADR36041;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Human nicking agent DNA containing BstNBI restriction site #2461.
XX
KW   ss; nicking agent; assay panel; diagnosis; expression pattern;
KW   DNA fingerprinting; nosocomial infection; microbiological assay;
KW   bacterial contamination; genome mapping; bioremediation.
XX
OS   Homo sapiens.
XX
PN   WO2004067765-A2.
XX
PD   12-AUG-2004.
XX
PF   29-JAN-2004; 2004WO-US002720.
XX
PR   29-JAN-2003; 2003US-0443811P.
XX
PA   (KECK-) KECK GRADUATE INST.
XX
PI   Van Ness J,  Galas DJ,  Van Ness LK;
XX
DR   WPI; 2004-581010/56.
XX
PT   Identifying nucleic acid sample source, useful for identifying bacterial
PT   strains involved in nosocomial infections, comprises treating the nucleic
PT   acid sample with components comprising a nicking agent under nicking
PT   conditions.
XX
PS   Example 3; Page 105-219; 238pp; English.
XX
CC   The invention relates to a method of treating a nucleic acid sample with
CC   components under nicking conditions, where the components comprise a
CC   nicking agent, and the conditions cause the nicking agent to nick the
CC   nucleic acid sample to thus produce a family of initiating
CC   oligonucleotide fragments, and subjecting one or more members of the
CC   family of initiating oligonucleotide fragments to a characterization
CC   process to thus provide results. The method is useful for creating an
CC   assay panel of diagnostic oligonucleotides that can identify any organism
CC   or individual. The method is useful for characterizing other DNA
CC   molecules e.g., cDNA, and for characterizing cDNA expression patterns.
CC   The method, kit or composition is useful for identifying the source
CC   organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC   non-human animal or human. The method is particularly useful for rapidly
CC   fingerprinting DNA to identifying prokaryotic and eukaryotic species,
CC   subspecies, and especially strains or individuals of the subspecies. It
CC   is especially useful for identifying different bacterial strains involved
CC   in e.g., nosocomial infections. Furthermore, the method is useful for
CC   diagnosing bacterial disease in plants and humans, monitoring for
CC   bacterial content and/or contamination in the environment, monitoring
CC   food for bacterial contamination, monitoring manufacturing processes for
CC   bacterial contamination, monitoring quality assurance/quality control of
CC   laboratory tests involving microbiological assays, tracing bacterial
CC   contamination and/or outbreaks of bacterial infections, genome mapping,
CC   monitoring bioremediation sites, and for monitoring agricultural sites
CC   for test crops, bacteria and recombinant molecules. Sequences ADR33581-
CC   ADR37496 correspond to target nucleic acids containing an NBstNBI
CC   restriction site and used in the method of the invention.
XX
SQ   Sequence 9 BP; 4 A; 1 C; 2 G; 1 T; 0 U; 1 Other;

  Query Match             20.0%;  Score 4;  DB 1;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 2.5e+02;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 CAGTCT 13
              :|| ||
Db          3 SAGACT 8


RESULT 124
ADR36040
ID   ADR36040 standard; DNA; 9 BP.
XX
AC   ADR36040;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Human nicking agent DNA containing BstNBI restriction site #2460.
XX
KW   ss; nicking agent; assay panel; diagnosis; expression pattern;
KW   DNA fingerprinting; nosocomial infection; microbiological assay;
KW   bacterial contamination; genome mapping; bioremediation.
XX
OS   Homo sapiens.
XX
PN   WO2004067765-A2.
XX
PD   12-AUG-2004.
XX
PF   29-JAN-2004; 2004WO-US002720.
XX
PR   29-JAN-2003; 2003US-0443811P.
XX
PA   (KECK-) KECK GRADUATE INST.
XX
PI   Van Ness J,  Galas DJ,  Van Ness LK;
XX
DR   WPI; 2004-581010/56.
XX
PT   Identifying nucleic acid sample source, useful for identifying bacterial
PT   strains involved in nosocomial infections, comprises treating the nucleic
PT   acid sample with components comprising a nicking agent under nicking
PT   conditions.
XX
PS   Example 3; Page 105-219; 238pp; English.
XX
CC   The invention relates to a method of treating a nucleic acid sample with
CC   components under nicking conditions, where the components comprise a
```

CC nicking agent, and the conditions cause the nicking agent to nick the
CC nucleic acid sample to thus produce a family of initiating
CC oligonucleotide fragments, and subjecting one or more members of the
CC family of initiating oligonucleotide fragments to a characterization
CC process to thus provide results. The method is useful for creating an
CC assay panel of diagnostic oligonucleotides that can identify any organism
CC or individual. The method is useful for characterizing other DNA
CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
CC The method, kit or composition is useful for identifying the source
CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC non-human animal or human. The method is particularly useful for rapidly
CC fingerprinting DNA to identifying prokaryotic and eukaryotic species,
CC subspecies, and especially strains or individuals of the subspecies. It
CC is especially useful for identifying different bacterial strains involved
CC in e.g., nosocomial infections. Furthermore, the method is useful for
CC diagnosing bacterial disease in plants and humans, monitoring for
CC bacterial content and/or contamination in the environment, monitoring
CC food for bacterial contamination, monitoring manufacturing processes for
CC bacterial contamination, monitoring quality assurance/quality control of
CC laboratory tests involving microbiological assays, tracing bacterial
CC contamination and/or outbreaks of bacterial infections, genome mapping,
CC monitoring bioremediation sites, and for monitoring agricultural sites
CC for test crops, bacteria and recombinant molecules. Sequences ADR33581-
CC ADR37496 correspond to target nucleic acids containing an NBstNBI
CC restriction site and used in the method of the invention.
XX
SQ Sequence 9 BP; 4 A; 1 C; 2 G; 1 T; 0 U; 1 Other;

```
  Query Match             20.0%;  Score 4;  DB 1;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 2.5e+02;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 CAGTCT 13
              :|| ||
Db          3 SAGACT 8
```

RESULT 125
ABV69205/c
ID ABV69205 standard; cDNA; 11 BP.
XX
AC ABV69205;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 6991.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 219; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 2 A; 4 C; 2 G; 3 T; 0 U; 0 Other;

```
  Query Match             20.0%;  Score 4;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CAGT 11
              ||||
Db          4 CAGT 1
```

RESULT 126
AAS98827
ID AAS98827 standard; DNA; 10 BP.
XX
AC AAS98827;
XX
DT 26-MAR-2002 (first entry)
XX
DE Colony stimulating factor 1 receptor (CSF1R) oligonucleotide #193.
XX
KW Colony stimulating factor 1 receptor; CSF1R; polymorphic variant;
KW cytostatic; gene therapy; malignant histiocytosis; isogene;
KW myeloid malignancy; inflammatory disorder; transgenic animal; haplotype;
KW genotype; human; allele specific oligonucleotide; ASO; primer;
KW primer extension; ss.
XX
OS Homo sapiens.
XX
PN WO200179225-A2.
XX
PD 25-OCT-2001.
XX
PF 12-APR-2001; 2001WO-US012044.
XX
PR 12-APR-2000; 2000US-0196411P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Chew A, Choi JY, Koshy B;
XX
DR WPI; 2002-075058/10.
XX
PT Novel polymorphic variants of colony stimulating factor 1 receptor useful
PT in studying expression and function of the protein, useful for screening
PT candidate drugs to treat diseases e.g. inflammatory disorders.
XX
PS Claim 17; Page 17; 164pp; English.
XX
CC The invention describes a novel isolated polynucleotide (I) comprising a
CC sequence which is a polymorphic variant (PV) of a reference sequence for
CC colony stimulating factor 1 receptor (CSF1R) gene, found on The
CC polypeptide are useful for improving the discovery and development of
CC drugs for treating diseases associated with CSF1R activity, e.g.,
CC malignant histiocytosis, myeloid malignancies, and inflammatory disorders
CC and the haplotypes can be used to validate CSF1R as a candidate target
CC for treating a specific condition or disease predicted to be associated
CC with CSF1R activity. Genotyping the CSF1R gene of an individual can also
CC be used in developing diagnostic tests and therapeutic treatments. (I) is
CC useful in studying the expression and function of CSF1R, and in

```
CC   expressing CSF1R protein for use in screening for candidate drugs to
CC   treat diseases related to CSF1R activity and in studying the effect of
CC   the variation on the biological activity of CSF1R as well as on the
CC   binding affinity of candidate drugs targeting CSF1R. Antibodies are
CC   useful in a variety of diagnostic and prognostic formats and therapeutic
CC   methods. A transgenic animal is useful in studying expression of the
CC   CSF1R isogenes in vivo, for in vivo screening and testing of drugs
CC   targeted against CSF1R protein, and for testing the efficacy of
CC   therapeutic agents and compounds. Allele specific oligonucleotides (ASO)
CC   are useful as probes and primers, and for assaying a polymorphism in the
CC   target region. Without requiring any a priori knowledge of the phenotypic
CC   effect of any particular CSF1R or haplotype the invention provides a
CC   method for identifying lead compounds that are more likely to show
CC   efficacy in clinical trials. This sequence is a primer used to detect
CC   CSF1R gene polymorphisms by primer extension, described in the method of
CC   the invention
XX
SQ   Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             18.0%;  Score 3.6;  DB 1;  Length 10;
  Best Local Similarity   60.0%;  Pred. No. 1.5e+02;
  Matches    6;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAGTC 12
              | ||  || | |
Db          1 GCCTGGAGAC 10


RESULT 127
ABV66235/c
ID   ABV66235 standard; cDNA; 11 BP.
XX
AC   ABV66235;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 4021.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 136; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 1 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             18.0%;  Score 3.6;  DB 1;  Length 11;
  Best Local Similarity   60.0%;  Pred. No. 1.5e+02;
  Matches    6;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          5 CTCCAGTCTC 14
              ||  || | |
Db         11 CTGGAGACAC 2


RESULT 128
ADP69107/c
ID   ADP69107 standard; DNA; 20 BP.
XX
AC   ADP69107;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human mitoNEET-specific antisense oligonucleotide #1.
XX
KW   human; antisense oligonucleotide; mitochondrial membrane;
KW   insulin sensitising antidiabetic thiazolodinediones; mitoNEET; diabetes;
KW   immunological disorder; cardiovascular disorder; including hypertension;
KW   neurological disorders; ischaemia; reperfusion; ss;
KW   2'-methoxyethyl gapmer; 2'-MOE gapmer; phosphorothioate backbone.
XX
OS   Homo sapiens.
XX
PN   WO2004053060-A2.
XX
PD   24-JUN-2004.
XX
PF   25-NOV-2003; 2003WO-US037621.
XX
PR   06-DEC-2002; 2002US-0431529P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Colca JR;
XX
DR   WPI; 2004-468836/44.
XX
PT   New antisense oligonucleotides encoding mitoNEET, useful for modulating
PT   mitoNEET expression or for treating diseases associated with mitoNEET,
PT   e.g. diabetes, immunological disorders or cardiovascular disorders.
XX
PS   Claim 4; SEQ ID NO 1; 226pp; English.
XX
CC   The invention comprises antisense oligonucleotides that are targeted to
CC   the nucleic acids encoding a family of human proteins from mitochondrial
CC   membranes, which bind insulin sensitising, antidiabetic
CC   thiazolodinediones (referred to as: mitoNEET). The antisense
CC   oligonucleotides of the invention are useful for modulating mitoNEET
CC   expression and for treating diseases or conditions associated with
CC   mitoNEET, such as: diabetes, immunological disorders, cardiovascular
CC   disorders including hypertension, neurological disorders, and
CC   ischaemia/reperfusion injuries. The present DNA sequence represents a
CC   mitoNEET-specific antisense oligonucleotide of the invention. NOTE: The
CC   present sequence is a 2'-methoxyethyl (2'-MOE) gapmer with a
CC   phosphorothioate backbone.
XX
SQ   Sequence 20 BP; 1 A; 6 C; 3 G; 10 T; 0 U; 0 Other;

  Query Match             18.0%;  Score 3.6;  DB 1;  Length 20;
  Best Local Similarity   60.0%;  Pred. No. 1.1e+02;
  Matches    6;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAGTC 12
```

```
                | ||  || |
Db         12 GACTGGAGAC 3


RESULT 129
ADP69109/c
ID   ADP69109 standard; DNA; 20 BP.
XX
AC   ADP69109;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human mitoNEET-specific antisense oligonucleotide #3.
XX
KW   human; antisense oligonucleotide; mitochondrial membrane;
KW   insulin sensitising antidiabetic thiazolodinediones; mitoNEET; diabetes;
KW   immunological disorder; cardiovascular disorder; including hypertension;
KW   neurological disorders; ischaemia; reperfusion; ss;
KW   2'-methoxyethyl gapmer; 2'-MOE gapmer; phosphorothioate backbone.
XX
OS   Homo sapiens.
XX
PN   WO2004053060-A2.
XX
PD   24-JUN-2004.
XX
PF   25-NOV-2003; 2003WO-US037621.
XX
PR   06-DEC-2002; 2002US-0431529P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Colca JR;
XX
DR   WPI; 2004-468836/44.
XX
PT   New antisense oligonucleotides encoding mitoNEET, useful for modulating
PT   mitoNEET expression or for treating diseases associated with mitoNEET,
PT   e.g. diabetes, immunological disorders or cardiovascular disorders.
XX
PS   Claim 4; SEQ ID NO 3; 226pp; English.
XX
CC   The invention comprises antisense oligonucleotides that are targeted to
CC   the nucleic acids encoding a family of human proteins from mitochondrial
CC   membranes, which bind insulin sensitising, antidiabetic
CC   thiazolodinediones (referred to as: mitoNEET). The antisense
CC   oligonucleotides of the invention are useful for modulating mitoNEET
CC   expression and for treating diseases or conditions associated with
CC   mitoNEET, such as: diabetes, immunological disorders, cardiovascular
CC   disorders including hypertension, neurological disorders, and
CC   ischaemia/reperfusion injuries. The present DNA sequence represents a
CC   mitoNEET-specific antisense oligonucleotide of the invention. NOTE: The
CC   present sequence is a 2'-methoxyethyl (2'-MOE) gapmer with a
CC   phosphorothioate backbone.
XX
SQ   Sequence 20 BP; 2 A; 6 C; 3 G; 9 T; 0 U; 0 Other;

  Query Match             18.0%;  Score 3.6;  DB 1;  Length 20;
  Best Local Similarity   60.0%;  Pred. No. 1.1e+02;
  Matches    6;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAGTC 12
              | ||  || |
Db         11 GACTGGAGAC 2


RESULT 130
ADP69110/c
ID   ADP69110 standard; DNA; 20 BP.
XX
AC   ADP69110;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human mitoNEET-specific antisense oligonucleotide #4.
XX
KW   human; antisense oligonucleotide; mitochondrial membrane;
KW   insulin sensitising antidiabetic thiazolodinediones; mitoNEET; diabetes;
KW   immunological disorder; cardiovascular disorder; including hypertension;
KW   neurological disorders; ischaemia; reperfusion; ss;
KW   2'-methoxyethyl gapmer; 2'-MOE gapmer; phosphorothioate backbone.
XX
OS   Homo sapiens.
XX
PN   WO2004053060-A2.
XX
PD   24-JUN-2004.
XX
PF   25-NOV-2003; 2003WO-US037621.
XX
PR   06-DEC-2002; 2002US-0431529P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Colca JR;
XX
DR   WPI; 2004-468836/44.
XX
PT   New antisense oligonucleotides encoding mitoNEET, useful for modulating
PT   mitoNEET expression or for treating diseases associated with mitoNEET,
PT   e.g. diabetes, immunological disorders or cardiovascular disorders.
XX
PS   Claim 4; SEQ ID NO 4; 226pp; English.
XX
CC   The invention comprises antisense oligonucleotides that are targeted to
CC   the nucleic acids encoding a family of human proteins from mitochondrial
CC   membranes, which bind insulin sensitising, antidiabetic
CC   thiazolodinediones (referred to as: mitoNEET). The antisense
CC   oligonucleotides of the invention are useful for modulating mitoNEET
CC   expression and for treating diseases or conditions associated with
CC   mitoNEET, such as: diabetes, immunological disorders, cardiovascular
CC   disorders including hypertension, neurological disorders, and
CC   ischaemia/reperfusion injuries. The present DNA sequence represents a
CC   mitoNEET-specific antisense oligonucleotide of the invention. NOTE: The
CC   present sequence is a 2'-methoxyethyl (2'-MOE) gapmer with a
CC   phosphorothioate backbone.
XX
SQ   Sequence 20 BP; 2 A; 6 C; 3 G; 9 T; 0 U; 0 Other;

  Query Match             18.0%;  Score 3.6;  DB 1;  Length 20;
  Best Local Similarity   60.0%;  Pred. No. 1.1e+02;
  Matches    6;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAGTC 12
              | ||  || |
Db         13 GACTGGAGAC 4


RESULT 131
ADP69108/c
ID   ADP69108 standard; DNA; 20 BP.
XX
AC   ADP69108;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human mitoNEET-specific antisense oligonucleotide #2.
XX
KW   human; antisense oligonucleotide; mitochondrial membrane;
KW   insulin sensitising antidiabetic thiazolodinediones; mitoNEET; diabetes;
KW   immunological disorder; cardiovascular disorder; including hypertension;
KW   neurological disorders; ischaemia; reperfusion; ss;
KW   2'-methoxyethyl gapmer; 2'-MOE gapmer; phosphorothioate backbone.
XX
OS   Homo sapiens.
XX
```

PN WO2004053060-A2.
XX
PD 24-JUN-2004.
XX
PF 25-NOV-2003; 2003WO-US037621.
XX
PR 06-DEC-2002; 2002US-0431529P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Colca JR;
XX
DR WPI; 2004-468836/44.
XX
PT New antisense oligonucleotides encoding mitoNEET, useful for modulating
PT mitoNEET expression or for treating diseases associated with mitoNEET,
PT e.g. diabetes, immunological disorders or cardiovascular disorders.
XX
PS Claim 4; SEQ ID NO 2; 226pp; English.
XX
CC The invention comprises antisense oligonucleotides that are targeted to
CC the nucleic acids encoding a family of human proteins from mitochondrial
CC membranes, which bind insulin sensitising, antidiabetic
CC thiazolodinediones (referred to as: mitoNEET). The antisense
CC oligonucleotides of the invention are useful for modulating mitoNEET
CC expression and for treating diseases or conditions associated with
CC mitoNEET, such as: diabetes, immunological disorders, cardiovascular
CC disorders including hypertension, neurological disorders, and
CC ischaemia/reperfusion injuries. The present DNA sequence represents a
CC mitoNEET-specific antisense oligonucleotide of the invention. NOTE: The
CC present sequence is a 2'-methoxyethyl (2'-MOE) gapmer with a
CC phosphorothioate backbone.
XX
SQ Sequence 20 BP; 2 A; 6 C; 3 G; 9 T; 0 U; 0 Other;

```
  Query Match             18.0%;  Score 3.6;  DB 1;  Length 20;
  Best Local Similarity   60.0%;  Pred. No. 1.1e+02;
  Matches    6;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAGTC 12
              | ||  || |
Db         10 GACTGGAGAC 1
```

RESULT 132
ADP69116/c
ID ADP69116 standard; DNA; 20 BP.
XX
AC ADP69116;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human mitoNEET-specific antisense oligonucleotide #10.
XX
KW human; antisense oligonucleotide; mitochondrial membrane;
KW insulin sensitising antidiabetic thiazolodinediones; mitoNEET; diabetes;
KW immunological disorder; cardiovascular disorder; including hypertension;
KW neurological disorders; ischaemia; reperfusion; ss;
KW 2'-methoxyethyl gapmer; 2'-MOE gapmer; phosphorothioate backbone.
XX
OS Homo sapiens.
XX
PN WO2004053060-A2.
XX
PD 24-JUN-2004.
XX
PF 25-NOV-2003; 2003WO-US037621.
XX
PR 06-DEC-2002; 2002US-0431529P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Colca JR;
XX
DR WPI; 2004-468836/44.
XX
PT New antisense oligonucleotides encoding mitoNEET, useful for modulating
PT mitoNEET expression or for treating diseases associated with mitoNEET,
PT e.g. diabetes, immunological disorders or cardiovascular disorders.
XX
PS Claim 4; SEQ ID NO 10; 226pp; English.
XX
CC The invention comprises antisense oligonucleotides that are targeted to
CC the nucleic acids encoding a family of human proteins from mitochondrial
CC membranes, which bind insulin sensitising, antidiabetic
CC thiazolodinediones (referred to as: mitoNEET). The antisense
CC oligonucleotides of the invention are useful for modulating mitoNEET
CC expression and for treating diseases or conditions associated with
CC mitoNEET, such as: diabetes, immunological disorders, cardiovascular
CC disorders including hypertension, neurological disorders, and
CC ischaemia/reperfusion injuries. The present DNA sequence represents a
CC mitoNEET-specific antisense oligonucleotide of the invention. NOTE: The
CC present sequence is a 2'-methoxyethyl (2'-MOE) gapmer with a
CC phosphorothioate backbone.
XX
SQ Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;

```
  Query Match             18.0%;  Score 3.6;  DB 1;  Length 20;
  Best Local Similarity   60.0%;  Pred. No. 1.1e+02;
  Matches    6;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAGTC 12
              | ||  || |
Db         14 GACTGGAGAC 5
```

RESULT 133
ADP69124/c
ID ADP69124 standard; DNA; 20 BP.
XX
AC ADP69124;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human mitoNEET-specific antisense oligonucleotide #18.
XX
KW human; antisense oligonucleotide; mitochondrial membrane;
KW insulin sensitising antidiabetic thiazolodinediones; mitoNEET; diabetes;
KW immunological disorder; cardiovascular disorder; including hypertension;
KW neurological disorders; ischaemia; reperfusion; ss;
KW 2'-methoxyethyl gapmer; 2'-MOE gapmer; phosphorothioate backbone.
XX
OS Homo sapiens.
XX
PN WO2004053060-A2.
XX
PD 24-JUN-2004.
XX
PF 25-NOV-2003; 2003WO-US037621.
XX
PR 06-DEC-2002; 2002US-0431529P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Colca JR;
XX
DR WPI; 2004-468836/44.
XX
PT New antisense oligonucleotides encoding mitoNEET, useful for modulating
PT mitoNEET expression or for treating diseases associated with mitoNEET,
PT e.g. diabetes, immunological disorders or cardiovascular disorders.
XX
PS Claim 4; SEQ ID NO 18; 226pp; English.
XX
CC The invention comprises antisense oligonucleotides that are targeted to
CC the nucleic acids encoding a family of human proteins from mitochondrial

```
CC   membranes, which bind insulin sensitising, antidiabetic
CC   thiazolodinediones (referred to as: mitoNEET). The antisense
CC   oligonucleotides of the invention are useful for modulating mitoNEET
CC   expression and for treating diseases or conditions associated with
CC   mitoNEET, such as: diabetes, immunological disorders, cardiovascular
CC   disorders including hypertension, neurological disorders, and
CC   ischaemia/reperfusion injuries. The present DNA sequence represents a
CC   mitoNEET-specific antisense oligonucleotide of the invention. NOTE: The
CC   present sequence is a 2'-methoxyethyl (2'-MOE) gapmer with a
CC   phosphorothioate backbone.
XX
SQ   Sequence 20 BP; 3 A; 7 C; 2 G; 8 T; 0 U; 0 Other;

  Query Match             18.0%;  Score 3.6;  DB 1;  Length 20;
  Best Local Similarity   60.0%;  Pred. No. 1.1e+02;
  Matches    6;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAGTC 12
              | ||  || |
Db         15 GACTGGAGAC 6


RESULT 134
ADP69130/c
ID   ADP69130 standard; DNA; 20 BP.
XX
AC   ADP69130;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human mitoNEET-specific antisense oligonucleotide #24.
XX
KW   human; antisense oligonucleotide; mitochondrial membrane;
KW   insulin sensitising antidiabetic thiazolodinediones; mitoNEET; diabetes;
KW   immunological disorder; cardiovascular disorder; including hypertension;
KW   neurological disorders; ischaemia; reperfusion; ss;
KW   2'-methoxyethyl gapmer; 2'-MOE gapmer; phosphorothioate backbone.
XX
OS   Homo sapiens.
XX
PN   WO2004053060-A2.
XX
PD   24-JUN-2004.
XX
PF   25-NOV-2003; 2003WO-US037621.
XX
PR   06-DEC-2002; 2002US-0431529P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Colca JR;
XX
DR   WPI; 2004-468836/44.
XX
PT   New antisense oligonucleotides encoding mitoNEET, useful for modulating
PT   mitoNEET expression or for treating diseases associated with mitoNEET,
PT   e.g. diabetes, immunological disorders or cardiovascular disorders.
XX
PS   Claim 4; SEQ ID NO 24; 226pp; English.
XX
CC   The invention comprises antisense oligonucleotides that are targeted to
CC   the nucleic acids encoding a family of human proteins from mitochondrial
CC   membranes, which bind insulin sensitising, antidiabetic
CC   thiazolodinediones (referred to as: mitoNEET). The antisense
CC   oligonucleotides of the invention are useful for modulating mitoNEET
CC   expression and for treating diseases or conditions associated with
CC   mitoNEET, such as: diabetes, immunological disorders, cardiovascular
CC   disorders including hypertension, neurological disorders, and
CC   ischaemia/reperfusion injuries. The present DNA sequence represents a
CC   mitoNEET-specific antisense oligonucleotide of the invention. NOTE: The
CC   present sequence is a 2'-methoxyethyl (2'-MOE) gapmer with a
CC   phosphorothioate backbone.
XX
SQ   Sequence 20 BP; 3 A; 7 C; 2 G; 8 T; 0 U; 0 Other;

  Query Match             18.0%;  Score 3.6;  DB 1;  Length 20;
  Best Local Similarity   60.0%;  Pred. No. 1.1e+02;
  Matches    6;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAGTC 12
              | ||  || |
Db         16 GACTGGAGAC 7


RESULT 135
AAZ81653/c
ID   AAZ81653 standard; DNA; 10 BP.
XX
AC   AAZ81653;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #887.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 82; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
```

```
CC   immunotherapy
XX
SQ   Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 U; 0 Other;

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 1.5e+02;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          9 AGACT 5


RESULT 136
ADU19570
ID   ADU19570 standard; DNA; 10 BP.
XX
AC   ADU19570;
XX
DT   13-JAN-2005  (first entry)
XX
DE   Hypoxia-related tumourigenesis-related SAGE tag #1361.
XX
KW   screening; hypoxia-related tumourigenesis;
KW   hypoxia-induced gene regulation; tumour; SAGE tag; ds.
XX
OS   Unidentified.
XX
PN   WO2004092198-A2.
XX
PD   28-OCT-2004.
XX
PF   09-APR-2004; 2004WO-US011087.
XX
PR   09-APR-2003; 2003US-0461712P.
XX
PA   (GENZ ) GENZYME CORP.
XX
PI   Nacht M;
XX
DR   WPI; 2004-758333/74.
XX
PT   Identifying agents that alter biological activity of a polypeptide
PT   encoded by a polynucleotide involved in hypoxia-related tumorigenesis
PT   comprises contacting an agent with a target cell and monitoring activity
PT   of expressed product.
XX
PS   Disclosure; Page 82; 100pp; English.
XX
CC   The invention comprises a method of screening for candidate agents
CC   capable of altering the biological activity of a protein encoded by a
CC   nucleotide involved in hypoxia-related tumourigenesis. The method of the
CC   invention involves: contacting a test agent with a target cell expressing
CC   the nucleotide, and monitoring the activity of the expressed protein
CC   product; if the test agent modifies the activity of the expressed protein
CC   then this is a candidate agent. The method of the invention is useful for
CC   modifying hypoxia-induced gene regulation and for diagnosing, prognosing
CC   or treating tumours. The present DNA sequence represents a SAGE tag that
CC   was used in the exemplification of the invention.
XX
SQ   Sequence 10 BP; 4 A; 1 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 1.5e+02;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          6 AGACT 10


RESULT 137
AAZ82947
ID   AAZ82947 standard; DNA; 10 BP.
XX
AC   AAZ82947;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #2181.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 118; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 1.5e+02;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          1 AGCCT 5
```

```
RESULT 138
AAZ83008/c
ID   AAZ83008 standard; DNA; 10 BP.
XX
AC   AAZ83008;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #2242.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 119; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 U; 0 Other;

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 1.5e+02;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          8 AGCCT 4
```

```
RESULT 139
AAZ86119
ID   AAZ86119 standard; DNA; 10 BP.
XX
AC   AAZ86119;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #5353.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 200; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 1.5e+02;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
```

```
              || ||
Db          2 AGACT 6


RESULT 140
AAF34179/c
ID   AAF34179 standard; DNA; 10 BP.
XX
AC   AAF34179;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:918.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 32; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 1 A; 3 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 1.5e+02;
    Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          8 AGACT 4


RESULT 141
AAF39592
ID   AAF39592 standard; DNA; 10 BP.
XX
AC   AAF39592;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6331.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 226; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 3 A; 1 C; 5 G; 1 T; 0 U; 0 Other;
```

```
  Query Match             17.0%;  Score 3.4;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 1.5e+02;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          3 AGGCT 7


RESULT 142
AAF38171/c
ID   AAF38171 standard; DNA; 10 BP.
XX
AC   AAF38171;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4910.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 175; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 U; 0 Other;

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 1.5e+02;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db         10 AGACT 6


RESULT 143
ACC41713
ID   ACC41713 standard; DNA; 10 BP.
XX
AC   ACC41713;
XX
DT   21-MAY-2003  (first entry)
XX
DE   Zinc finger protein DNA-binding domain target sequence SEQ ID NO:260.
XX
KW   Zinc finger domain; zinc finger; zinc finger binding domain; probe;
KW   chimeric nucleic acid; library; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO2003016571-A1.
XX
PD   27-FEB-2003.
XX
PF   17-AUG-2002; 2002WO-KR001560.
XX
PR   17-AUG-2001; 2001US-0313402P.
PR   22-APR-2002; 2002US-0374355P.
XX
PA   (TOOL-) TOOLGEN INC.
XX
PI   Kim J,  Bae K,  Park K,  Kwon Y,  Ryu E,  Hwang M;
XX
DR   WPI; 2003-268344/26.
XX
PT   New library comprising polypeptides having zinc finger domains, useful
PT   for producing chimeric nucleic acids.
XX
PS   Claim 40; Page 105; 234pp; English.
XX
CC   The present invention describes a library comprising polypeptides. Each
CC   polypeptide comprises a first or second zinc finger domain. The domains
CC   of each polypeptide are identical to a zinc finger domain from a
CC   naturally occurring protein and either do not occur in the same naturally
CC   occurring protein or occur in the same naturally occurring protein in a
CC   different configuration than in the polypeptide. The domains vary among
CC   polypeptides. Also described: (1) producing chimeric nucleic acids; (2)
CC   generating an artificial zinc finger polypeptide that specifically binds
CC   to a target DNA site; and (3) identifying a nucleic acid encoding a zinc
CC   finger polypeptide that specifically recognises a target DNA site. The
CC   library can be used for producing chimeric nucleic acids. ACC41551 to
CC   ACC41758 and ABR40919 to ABR41015 represent nucleotide and amino acid
CC   sequences given in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 5 A; 2 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 1.5e+02;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          6 AGACT 10
```

RESULT 144
ADZ67944
ID ADZ67944 standard; DNA; 10 BP.
XX
AC ADZ67944;
XX
DT 14-JUL-2005 (first entry)
XX
DE NTRK1 gene polymorphic site 8 primer extension oligonucleotide.
XX
KW Neurotrophic tyrosine kinase receptor type 1; NTRK1; Alzheimers disease;
KW neurological disease; diagnosis; prognosis; primer; SNP detection;
KW haplotype mapping; ss.
XX
OS Homo sapiens.
XX
PN WO2005037204-A2.
XX
PD 28-APR-2005.
XX
PF 14-OCT-2004; 2004WO-US033689.
XX
PR 15-OCT-2003; 2003US-0511247P.
XX
PA (GENA-) GENAISSANCE PHARM.
XX
PI Aerssens J, Athanasiou M, Brain C, Cohen N, Dain B, Denton RR;
PI Judson RS, Ozdemir V, Reed CR;
XX
DR WPI; 2005-322749/33.
XX
PT Determining whether individual has age of onset marker I or marker II, by
PT determining whether individual has zero copies or copy of neurotrophic
PT tyrosine kinase, receptor, type 1 haplotypes involved in onset of
PT Alzheimer's disease.
XX
PS Disclosure; SEQ ID NO 42; 128pp; English.
XX
CC The inventors have discovered a set of 112 haplotypes in the human
CC neurotrophic tyrosine kinase, receptor, type 1 (NTRK1) gene ADZ67903 that
CC are associated with the age of onset of Alzheimer's disease (AD). They
CC have also discovered that the copy number of each of these NTRK1
CC haplotypes affects the age of onset of AD. If an individual has at least
CC one copy of any of the 112 specified haplotypes, that individual is
CC defined as having an 'age of onset marker I' and is more likely to have a
CC later age of onset of AD than an individual having zero copies of any of
CC the 112 haplotypes, such an individual being defined as 'age of onset
CC marker II'. Testing for the presence or absence, and copy number, of the
CC haplotypes is useful for predicting the age at which individuals who are
CC at increased risk of AD are likely to develop AD and to help confirm a
CC diagnosis of mild or minimal cognitive impairment (MDI) or AD. Such
CC knowledge will assist therapy and lifestyle decisions. The correlation of
CC certain NTRK1 haplotypes with age of AD onset indicates that variation in
CC the NTKR1 gene should be considered in the development and clinical
CC trials of drugs for treating MCI, AD and other neurodegenerative
CC disorders. This correlation also provides a basis for pursuing NTRK1 as a
CC target for drugs designed to treat cognitive disorders such as MDI, AD
CC and other neurological diseases or conditions. Information is provided
CC about the composition of each of 112 haplotypes, namely the location in
CC the NTRK1 gene of each of the polymorphic sites (PSs) and the identity of
CC the reference and variant allele at each PS. An individual's genotype for
CC the set of PSs is obtained by primer extension, allele-specific PCR,
CC nucleic acid amplification, hybridization, mismatch detection, enzymatic
CC nucleic acid cleavage or sequencing assay. The present sequence is that
CC of a reverse primer extension oligonucleotide for detecting PS8 in
CC haplotypes comprising preferred embodiments of age of onset markers I and
CC II.
XX
SQ Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 17.0%; Score 3.4; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 AGTCT 13
|| ||
Db 2 AGACT 6

RESULT 145
AEA62012
ID AEA62012 standard; DNA; 10 BP.
XX
AC AEA62012;
XX
DT 11-AUG-2005 (first entry)
XX
DE NTRK1 gene polymorphic site 8 primer extension oligonucleotide.
XX
KW NTRK1 gene; neurotrophic tyrosine kinase, receptor, type 1;
KW Alzheimers disease; degeneration; neurological disease;
KW haplotype mapping; prognosis; primer; ss; SNP detection.
XX
OS Homo sapiens.
XX
PN WO2005052180-A2.
XX
PD 09-JUN-2005.
XX
PF 22-NOV-2004; 2004WO-US038876.
XX
PR 24-NOV-2003; 2003US-0524636P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Aerssens J, Athanasiou M, Brain C, Cohen N, Dain B, Denton RR;
PI Judson RS, Ozdemir V, Reed CR;
XX
DR WPI; 2005-418015/42.
XX
PT Determining whether an individual has a progression marker I or
PT progression marker II, useful for predicting an individual's progression
PT of Alzheimer's disease, by determining whether the individual has any of
PT the NTRK1 haplotypes.
XX
PS Claim 40; SEQ ID NO 53; 108pp; English.
XX
CC The present invention relates to genetic markers of the human
CC neurotrophic tyrosine kinase, receptor, type 1 (NTRK1) gene AEA61960 that
CC are associated with progression of Alzheimer's disease (AD). 12
CC Polymorphic sites (PSs) have been discovered in the NTRK1 gene of
CC Caucasian individuals with AD, and a set of 70 haplotypes having
CC association with progression of AD have been identified. If an individual
CC has 0 or 1 copy of any of haplotypes 1-41 and 67-70, or 0 copies of any
CC of haplotypes 42-66, then that individual is defined as having a
CC progression marker I and is more likely to exhibit a slower progression
CC of AD than an individual having 2 copies of any of haplotypes 1-41 and 67
CC -70, or at least 1 copy of any of haplotypes 42-66, such an individual
CC being defined as having a progression marker II. Additional haplotypes
CC may be identified that are in linkage disequilibrium with any of
CC haplotypes 1-70, referred to as linked haplotypes and substitute
CC haplotypes of any of haplotypes 1-70, in which one or more of the PSs in
CC the original haplotype is substituted with another PS, where the allele
CC at the substituted PS is in linkage disequilibrium with the allele at the
CC substituting PS. The invention provides methods and kits for determining
CC whether an individual has a progression marker I or a progression marker
CC II. A method is also provided for predicting an individual's progression
CC of AD. The individual is especially a Caucasian diagnosed as having a
CC cognitive disorder. An individual's genotype for each PS may be obtained
CC by primer extension, allele-specific PCR, nucleic acid amplification,
CC hybridization, mismatch-detection, enzymatic nucleic acid cleavage or
CC sequencing assay. The present sequence is a reverse primer extension
CC oligonucleotide that can be used to detect the allele at PS8 of the NTRK1
CC gene. The 3' terminus of the oligonucleotide is complementary to the
CC nucleotide located immediately adjacent to the PS. The oligonucleotide is
CC included in a claimed kit of the invention used to determine whether an

```
CC   individual has a progression marker I or progression marker II.
XX
SQ   Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 1.5e+02;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          2 AGACT 6


RESULT 146
AAZ83176
ID   AAZ83176 standard; DNA; 10 BP.
XX
AC   AAZ83176;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #2410.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 124; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 1.5e+02;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          4 AGACT 8


RESULT 147
AAH63895/c
ID   AAH63895 standard; cDNA; 10 BP.
XX
AC   AAH63895;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 735.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US031922.
XX
PR   24-NOV-1999;   99US-00448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell type,
PT   such as cancer cell, comprises transcriptomes expressed in particular
PT   cell types.
XX
PS   Claim 13; Page 56; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences AAH63161-
CC   AAH64724 is expressed by the cell. The transcriptomes described in the
CC   invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of the
CC   transcriptomes described in the exemplification of the invention
XX
SQ   Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 1.5e+02;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          6 AGACT 2


RESULT 148
AAF41988
ID   AAF41988 standard; DNA; 10 BP.
```

```
XX
AC   AAF41988;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8727.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 311; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 2 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 1.5e+02;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          2 AGACT 6
```

```
RESULT 149
AAD25917/c
ID   AAD25917 standard; DNA; 10 BP.
XX
AC   AAD25917;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Human MC4R gene polymorphism detecting primer #2.
XX
KW   Human; single nucleotide polymorphism; SNP; melanocortin 4-receptor;
KW   MC4R; haplotype; obesity; screening; allele-specific oligonucleotide;
KW   ASO; gene therapy; anorectic; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200179222-A2.
XX
PD   25-OCT-2001.
XX
PF   12-APR-2001; 2001WO-US011943.
XX
PR   12-APR-2000; 2000US-0196677P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Bentivegna SC,  Choi JY,  Kazemi A,  Lee HH,  Nandabalan K,  Parks KE;
PI   Sausker EA;
XX
DR   WPI; 2002-082744/11.
XX
PT   Novel polymorphic variants of melanocortin 4-receptor gene useful in
PT   studying expression and function of the protein, useful for screening
PT   candidate drugs to treat diseases related to the protein activity e.g.
PT   obesity.
XX
PS   Claim 17; Page 13; 53pp; English.
XX
CC   The invention relates to single nucleotide polymorphisms (SNP) in human
CC   melanocortin 4-receptor (MC4R) gene. MC4R gene haplotypes are useful for
CC   improving the efficiency and reliability of several steps in the
CC   discovery and development of drugs for treating diseases associated with
CC   MC4R activity, e.g. obesity. MC4R gene is useful in studying the
CC   expression and function of MC4R and in expressing MC4R protein for use in
CC   screening for candidate drugs to treat diseases related to MC4R activity
CC   and in studying the effect of the variation on the biological activity of
CC   MC4R as well as on the binding affinity of candidate drugs targetting
CC   MC4R for the treatment of obesity. MC4R antibody is useful in a variety
CC   of diagnostic and prognostic formats and in therapeutic methods. Allele-
CC   specific oligonucleotide (ASO) is useful as probes and primers, and for
CC   assaying a polymorphism in MC4R gene. MC4R DNA is used in gene therapy.
CC   The present sequence is a primer used to detect polymorphism in human
CC   MC4R gene
XX
SQ   Sequence 10 BP; 1 A; 2 C; 1 G; 6 T; 0 U; 0 Other;

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 1.5e+02;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          6 AGACT 2


RESULT 150
ABV78460
ID   ABV78460 standard; cDNA; 10 BP.
XX
AC   ABV78460;
XX
DT   29-NOV-2002  (first entry)
XX
```

```
DE   Human Th1 cell preferentially expressed EST SAGE tag, SEQ ID NO:171.
XX
KW   SAGE tag; serial analysis of gene expression; human; Th1 cell;
KW   activated T cell; T lymphocyte; immune response; expression pattern;
KW   preferential expression; immune disorder; EST; expressed sequence tag;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   JP2002186482-A.
XX
PD   02-JUL-2002.
XX
PF   19-DEC-2000; 2000JP-00385816.
XX
PR   19-DEC-2000; 2000JP-00385816.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2002-594261/64.
XX
PT   Human activated Th1 and Th2 cell expression gene group, useful for the
PT   diagnosis and treatment of Th1 and Th2-related diseases.
XX
PS   Claim 19; Page 11; 60pp; Japanese.
XX
CC   The invention relates to SAGE (serial analysis of gene expression) tags
CC   representing groups of genes which are expressed in activated human Th1
CC   and/or Th2 cells. The SAGE tags of this invention consist of a sequence
CC   of 10 nucleotides located downstream of the 5'-CATG-3' sequence motif
CC   lying nearest to the polyA region of cDNAs derived from a variety of
CC   genes. These tags serve to uniquely identify each transcript and can thus
CC   be used to analyse the pattern of gene expression in particular cell
CC   types. The invention also relates to proteins encoded by the genes
CC   expressed in Th1 and/or Th2 cells, antibodies against these proteins, and
CC   inhibitors of the expression of groups of genes that are expressed in
CC   either or both the two cell types. Groups of genes expressed in Th1
CC   and/or Th2 cell types may be used for the diagnosis and treatment of Th1
CC   and Th2-related disorders. Sequences ABV78390-ABV78560 are SAGE tags
CC   representing 171 genes which are more highly expressed in Th1 cells
CC   compared with Th2 cells
XX
SQ   Sequence 10 BP; 4 A; 1 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 1.5e+02;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          1 AGACT 5


RESULT 151
ABK23710/c
ID   ABK23710 standard; DNA; 10 BP.
XX
AC   ABK23710;
XX
DT   09-APR-2002  (first entry)
XX
DE   Transcript tag DNA sequence #299 induced or suppressed by N-myc.
XX
KW   Myc-dependent downstream gene; neoplastic; cancer; growth; invasion;
KW   spread; myc target; myc tag; SAGE; serial analysis of gene expression;
KW   myc oncogene; N-myc; human neuroblastoma; cytostatic; ds.
XX
OS   Homo sapiens.
XX
PN   WO200185941-A2.
XX
PD   15-NOV-2001.
XX
PF   11-MAY-2001; 2001WO-NL000361.
XX
PR   11-MAY-2000; 2000EP-00201698.
PR   29-JUN-2000; 2000EP-00202284.
XX
PA   (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.
XX
PI   Versteeg R,  Caron HN;
XX
DR   WPI; 2002-066603/09.
XX
PT   A new nucleic acid library of myc-dependent downstream genes capable of
PT   supporting a neoplastic characteristic of cancer is useful to find new
PT   therapies and diagnoses for cancer.
XX
PS   Disclosure; Page 57; 69pp; English.
XX
CC   The present invention relates to a nucleic acid library comprising myc-
CC   dependent downstream genes or their functional fragments essentially
CC   capable of supporting a neoplastic character of cancer such as growth,
CC   invasion or spread. These myc target or tag sequences are identified by
CC   SAGE (serial analysis of gene expression). The library is useful to find
CC   new diagnoses and treatments for cancer. The invention is also useful to
CC   enhance production of recombinant proteins in a production system with
CC   high expression of endogenous or transfected myc oncogenes. ABK23412-
CC   ABK23828 represent transcript tag DNA sequences that are activated or
CC   repressed by N-myc in human neuroblastoma
XX
SQ   Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 1.5e+02;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          6 AGACT 2


RESULT 152
ADA00650/c
ID   ADA00650 standard; DNA; 10 BP.
XX
AC   ADA00650;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Oligonucleotide microchip associated probe #3.
XX
KW   discrete porous entity; microchip; cross contamination;
KW   chemical communication; co-polymerisation; ss; probe.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag= a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= Fluorescein"
XX
PN   US2003036063-A1.
XX
PD   20-FEB-2003.
XX
PF   15-AUG-2001; 2001US-00930865.
XX
PR   15-AUG-2001; 2001US-00930865.
XX
PA   (MIRZ/) MIRZABEKOV A.
PA   (TIMO/) TIMOFEEV E.
PA   (VASI/) VASILISKOV V.
XX
PI   Mirzabekov A,  Timofeev E,  Vasiliskov V;
```

```
XX
DR   WPI; 2003-605713/57.
XX
PT   Making discrete porous entities containing synthetic and natural
PT   compounds, useful as biochips, involves contacting each molecule at
PT   individual positions on insert substrate with compound, and solidifying
PT   the formed individual mixtures.
XX
PS   Example 2; Fig 5; 11pp; English.
XX
CC   The invention describes a method of making discrete porous entities that
CC   each contain a different molecule. The method comprises: positioning each
CC   different molecule at individual positions on an inert substrate;
CC   contacting each positioned molecule with compound to form individual
CC   mixtures; and solidifying the mixtures. The inventive method provides
CC   microchips that minimise any chance for cross contamination and chemical
CC   communication between entities. The contents of the entities do not mix
CC   with each other. It provides microchips having higher sensitivity and
CC   much faster kinetics of hybridisation. It facilitates the production of
CC   co-polymerised gel pads that can be as small as 3 x 3 microns. This
CC   sequence represents a associated with a oligonucleotide microchip
CC   prepared by photoinduced simultaneous co-polymerisation of 4 allyl-
CC   oligonucleotides.
XX
SQ   Sequence 10 BP; 1 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 1.5e+02;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          9 AGACT 5


RESULT 153
ABV64201
ID   ABV64201 standard; cDNA; 11 BP.
XX
AC   ABV64201;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 1987.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 80; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 3 A; 1 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 11;
  Best Local Similarity   80.0%;  Pred. No. 1.6e+02;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          5 AGGCT 9


RESULT 154
ABV71622
ID   ABV71622 standard; cDNA; 11 BP.
XX
AC   ABV71622;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 9408.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Claim 24; Page 303; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 3 A; 1 C; 6 G; 1 T; 0 U; 0 Other;
```

```
  Query Match            17.0%;  Score 3.4;  DB 1;  Length 11;
  Best Local Similarity  80.0%;  Pred. No. 1.6e+02;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          5 AGGCT 9


RESULT 155
ABQ87397
ID   ABQ87397 standard; cDNA; 11 BP.
XX
AC   ABQ87397;
XX
DT   10-SEP-2002  (first entry)
XX
DE   Human skin stress/ageing related EST SEQ ID NO 1152.
XX
KW   Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253773-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015178.
XX
PR   03-JAN-2001; 2001DE-01000121.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-528865/56.
XX
PT   Identifying genes involved in skin stress and aging, useful e.g. in
PT   screening for cosmetic or therapeutic agents, based on differential gene
PT   expression.
XX
PS   Claim 8; Page 85; 325pp; German.
XX
CC   The invention relates to identifying (M1) genes in vitro that, in humans
CC   or animals, are important for skin ageing and/or skin stress by serial
CC   analysis of gene expression between mixtures of transcribed and
CC   optionally translated, genetically encoded factors (A) obtained from
CC   young and aged skin, to identify that genes that show strong differential
CC   expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC   useful for: identifying markers of skin ageing and/or stress; determining
CC   skin ageing and/or stress; and identifying or determining the effects of
CC   pharmaceutical or cosmetic agents for control of skin ageing. The present
CC   sequence is one of a group of human skin ageing/stress related expressed
CC   sequence tags (ABQ86246-ABQ87680) of the invention
XX
SQ   Sequence 11 BP; 4 A; 1 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match            17.0%;  Score 3.4;  DB 1;  Length 11;
  Best Local Similarity  80.0%;  Pred. No. 1.6e+02;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          6 AGACT 10


RESULT 156
ABV65400
ID   ABV65400 standard; cDNA; 11 BP.
XX
AC   ABV65400;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 3186.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 113; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 4 A; 1 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match            17.0%;  Score 3.4;  DB 1;  Length 11;
  Best Local Similarity  80.0%;  Pred. No. 1.6e+02;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          6 AGACT 10


RESULT 157
ABN09352
ID   ABN09352 standard; DNA; 17 BP.
XX
AC   ABN09352;
XX
DT   29-MAY-2002  (first entry)
XX
DE   Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9344.
XX
KW   Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW   muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW   skeletal muscle disorder; amplicon; screening; ss.
XX
OS   Homo sapiens.
XX
PN   WO200192524-A2.
XX
PD   06-DEC-2001.
XX
```

```
PF   25-MAY-2001; 2001WO-US016981.
XX
PR   26-MAY-2000; 2000US-0207456P.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
PR   30-JAN-2001; 2001WO-US000661.
PR   30-JAN-2001; 2001WO-US000662.
PR   30-JAN-2001; 2001WO-US000663.
PR   30-JAN-2001; 2001WO-US000664.
PR   30-JAN-2001; 2001WO-US000665.
PR   30-JAN-2001; 2001WO-US000666.
PR   30-JAN-2001; 2001WO-US000667.
PR   30-JAN-2001; 2001WO-US000668.
PR   30-JAN-2001; 2001WO-US000669.
PR   30-JAN-2001; 2001WO-US000670.
PR   05-FEB-2001; 2001US-0266860P.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Gu Y,  Ji Y,  Penn SG,  Hanzel DK,  Rank DR,  Chen W,  Shannon ME;
XX
DR   WPI; 2002-179446/23.
XX
PT   New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT   or as specific biomolecule capture probes for surface-enhanced laser
PT   desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
PS   Disclosure; SEQ ID NO 9344; 214pp; English.
XX
CC   The present invention describes a human genome-derived myosin-like
CC   protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC   1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC   nucleic acids can be used as probes to detect, characterise and quantify
CC   hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC   provide initial substrates for the recombinant engineering of hGDMLP-1
CC   protein variants having desired phenotypic improvements, and for
CC   expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC   used as immunogens to raise antibodies that specifically recognise hGDMLP
CC   -1 proteins, as standards in assays used to determine the concentration
CC   and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC   capture probes for surface-enhanced laser desorption ionisation, as
CC   therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC   production, and in vaccines or for replacement therapy. The
CC   polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC   disorder associated with the expression of hGDMLP-1, in particular heart
CC   and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC   The present sequence represents an oligomer used in the screening of the
CC   hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequence
XX
SQ   Sequence 17 BP; 6 A; 2 C; 8 G; 1 T; 0 U; 0 Other;

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 17;
  Best Local Similarity   80.0%;  Pred. No. 1.3e+02;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          8 AGGCT 12


RESULT 158
ABN09353
ID   ABN09353 standard; DNA; 17 BP.
XX
AC   ABN09353;
XX
DT   29-MAY-2002  (first entry)
XX
DE   Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9345.
XX
KW   Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW   muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW   skeletal muscle disorder; amplicon; screening; ss.
XX
OS   Homo sapiens.
XX
PN   WO200192524-A2.
XX
PD   06-DEC-2001.
XX
PF   25-MAY-2001; 2001WO-US016981.
XX
PR   26-MAY-2000; 2000US-0207456P.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
PR   30-JAN-2001; 2001WO-US000661.
PR   30-JAN-2001; 2001WO-US000662.
PR   30-JAN-2001; 2001WO-US000663.
PR   30-JAN-2001; 2001WO-US000664.
PR   30-JAN-2001; 2001WO-US000665.
PR   30-JAN-2001; 2001WO-US000666.
PR   30-JAN-2001; 2001WO-US000667.
PR   30-JAN-2001; 2001WO-US000668.
PR   30-JAN-2001; 2001WO-US000669.
PR   30-JAN-2001; 2001WO-US000670.
PR   05-FEB-2001; 2001US-0266860P.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Gu Y,  Ji Y,  Penn SG,  Hanzel DK,  Rank DR,  Chen W,  Shannon ME;
XX
DR   WPI; 2002-179446/23.
XX
PT   New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT   or as specific biomolecule capture probes for surface-enhanced laser
PT   desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
PS   Disclosure; SEQ ID NO 9345; 214pp; English.
XX
CC   The present invention describes a human genome-derived myosin-like
CC   protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC   1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC   nucleic acids can be used as probes to detect, characterise and quantify
CC   hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC   provide initial substrates for the recombinant engineering of hGDMLP-1
CC   protein variants having desired phenotypic improvements, and for
CC   expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC   used as immunogens to raise antibodies that specifically recognise hGDMLP
CC   -1 proteins, as standards in assays used to determine the concentration
CC   and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC   capture probes for surface-enhanced laser desorption ionisation, as
CC   therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC   production, and in vaccines or for replacement therapy. The
CC   polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC   disorder associated with the expression of hGDMLP-1, in particular heart
CC   and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC   The present sequence represents an oligomer used in the screening of the
CC   hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequence
XX
SQ   Sequence 17 BP; 5 A; 3 C; 8 G; 1 T; 0 U; 0 Other;

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 17;
  Best Local Similarity   80.0%;  Pred. No. 1.3e+02;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          7 AGGCT 11
```

```
RESULT 159
ABN09354
ID   ABN09354 standard; DNA; 17 BP.
XX
AC   ABN09354;
XX
DT   29-MAY-2002  (first entry)
XX
DE   Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9346.
XX
KW   Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW   muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW   skeletal muscle disorder; amplicon; screening; ss.
XX
OS   Homo sapiens.
XX
PN   WO200192524-A2.
XX
PD   06-DEC-2001.
XX
PF   25-MAY-2001; 2001WO-US016981.
XX
PR   26-MAY-2000; 2000US-0207456P.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
PR   30-JAN-2001; 2001WO-US000661.
PR   30-JAN-2001; 2001WO-US000662.
PR   30-JAN-2001; 2001WO-US000663.
PR   30-JAN-2001; 2001WO-US000664.
PR   30-JAN-2001; 2001WO-US000665.
PR   30-JAN-2001; 2001WO-US000666.
PR   30-JAN-2001; 2001WO-US000667.
PR   30-JAN-2001; 2001WO-US000668.
PR   30-JAN-2001; 2001WO-US000669.
PR   30-JAN-2001; 2001WO-US000670.
PR   05-FEB-2001; 2001US-0266860P.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Gu Y,  Ji Y,  Penn SG,  Hanzel DK,  Rank DR,  Chen W,  Shannon ME;
XX
DR   WPI; 2002-179446/23.
XX
PT   New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT   or as specific biomolecule capture probes for surface-enhanced laser
PT   desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
PS   Disclosure; SEQ ID NO 9346; 214pp; English.
XX
CC   The present invention describes a human genome-derived myosin-like
CC   protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC   1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC   nucleic acids can be used as probes to detect, characterise and quantify
CC   hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC   provide initial substrates for the recombinant engineering of hGDMLP-1
CC   protein variants having desired phenotypic improvements, and for
CC   expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC   used as immunogens to raise antibodies that specifically recognise hGDMLP
CC   -1 proteins, as standards in assays used to determine the concentration
CC   and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC   capture probes for surface-enhanced laser desorption ionisation, as
CC   therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC   production, and in vaccines or for replacement therapy. The
CC   polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC   disorder associated with the expression of hGDMLP-1, in particular heart
CC   and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC   The present sequence represents an oligomer used in the screening of the
CC   hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequence
XX
SQ   Sequence 17 BP; 5 A; 3 C; 8 G; 1 T; 0 U; 0 Other;

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 17;
  Best Local Similarity   80.0%;  Pred. No. 1.3e+02;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          6 AGGCT 10


RESULT 160
ACN72443
ID   ACN72443 standard; DNA; 17 BP.
XX
AC   ACN72443;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Human GDMLP-1 probe SEQ ID NO:9345.
XX
KW   Human; ss; probe; myosin-like protein-1; hGDMLP-1;
KW   hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
KW   skeletal muscle function.
XX
OS   Homo sapiens.
XX
PN   US2004137589-A1.
XX
PD   15-JUL-2004.
XX
PF   26-NOV-2003; 2003US-00723361.
XX
PR   26-MAY-2000; 2000US-0207456P.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
PR   30-JAN-2001; 2001WO-US000661.
PR   30-JAN-2001; 2001WO-US000662.
PR   30-JAN-2001; 2001WO-US000663.
PR   30-JAN-2001; 2001WO-US000664.
PR   30-JAN-2001; 2001WO-US000665.
PR   30-JAN-2001; 2001WO-US000666.
PR   30-JAN-2001; 2001WO-US000667.
PR   30-JAN-2001; 2001WO-US000668.
PR   30-JAN-2001; 2001WO-US000669.
PR   30-JAN-2001; 2001WO-US000670.
PR   05-FEB-2001; 2001US-0266860P.
PR   25-MAY-2001; 2001US-00866108.
XX
PA   (GUYY/) GU Y.
PA   (JIYY/) JI Y.
PA   (PENN/) PENN S G.
PA   (HANZ/) HANZEL D K.
PA   (RANK/) RANK D.
PA   (CHEN/) CHEN W.
PA   (SHAN/) SHANNON M E.
XX
PI   Gu Y,  Ji Y,  Penn SG,  Hanzel DK,  Rank D,  Chen W,  Shannon ME;
XX
DR   WPI; 2004-533378/51.
XX
PT   Novel myosin-like protein-1, useful for treating or preventing disorder
PT   associated with decreased expression or activity of human genome-derived
PT   myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT   function.
XX
PS   Disclosure; SEQ ID NO 9345; 0pp; English.
XX
CC   The invention relates to a novel polypeptide (I) comprising a sequence
CC   (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully
```

```
CC   defined in the specification, a fragment of at least 8 amino acids of
CC   (S1), 95% deviation from (S1) which are conservative substitutions, and
CC   65% identity to (S1). A polypeptide of the invention acts as a agonist or
CC   antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A
CC   pharmaceutical composition of the invention is useful for treating or
CC   preventing a disorder associated with decreased expression or activity of
CC   hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
CC   The present sequence represents a 17-mer nucleotide, used in the
CC   invention for scanning the sequence represented in ACN63103
XX
SQ   Sequence 17 BP; 5 A; 3 C; 8 G; 1 T; 0 U; 0 Other;

  Query Match            17.0%;  Score 3.4;  DB 1;  Length 17;
  Best Local Similarity   80.0%;  Pred. No. 1.3e+02;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          7 AGGCT 11


RESULT 161
ACN72442
ID   ACN72442 standard; DNA; 17 BP.
XX
AC   ACN72442;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Human GDMLP-1 probe SEQ ID NO:9344.
XX
KW   Human; ss; probe; myosin-like protein-1; hGDMLP-1;
KW   hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
KW   skeletal muscle function.
XX
OS   Homo sapiens.
XX
PN   US2004137589-A1.
XX
PD   15-JUL-2004.
XX
PF   26-NOV-2003; 2003US-00723361.
XX
PR   26-MAY-2000; 2000US-0207456P.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
PR   30-JAN-2001; 2001WO-US000661.
PR   30-JAN-2001; 2001WO-US000662.
PR   30-JAN-2001; 2001WO-US000663.
PR   30-JAN-2001; 2001WO-US000664.
PR   30-JAN-2001; 2001WO-US000665.
PR   30-JAN-2001; 2001WO-US000666.
PR   30-JAN-2001; 2001WO-US000667.
PR   30-JAN-2001; 2001WO-US000668.
PR   30-JAN-2001; 2001WO-US000669.
PR   30-JAN-2001; 2001WO-US000670.
PR   05-FEB-2001; 2001US-0266860P.
PR   25-MAY-2001; 2001US-00866108.
XX
PA   (GUYY/) GU Y.
PA   (JIYY/) JI Y.
PA   (PENN/) PENN S G.
PA   (HANZ/) HANZEL D K.
PA   (RANK/) RANK D.
PA   (CHEN/) CHEN W.
PA   (SHAN/) SHANNON M E.
XX
PI   Gu Y,  Ji Y,  Penn SG,  Hanzel DK,  Rank D,  Chen W,  Shannon ME;
XX
DR   WPI; 2004-533378/51.
XX
PT   Novel myosin-like protein-1, useful for treating or preventing disorder
PT   associated with decreased expression or activity of human genome-derived
PT   myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT   function.
XX
PS   Disclosure; SEQ ID NO 9344; 0pp; English.
XX
CC   The invention relates to a novel polypeptide (I) comprising a sequence
CC   (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully
CC   defined in the specification, a fragment of at least 8 amino acids of
CC   (S1), 95% deviation from (S1) which are conservative substitutions, and
CC   65% identity to (S1). A polypeptide of the invention acts as a agonist or
CC   antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A
CC   pharmaceutical composition of the invention is useful for treating or
CC   preventing a disorder associated with decreased expression or activity of
CC   hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
CC   The present sequence represents a 17-mer nucleotide, used in the
CC   invention for scanning the sequence represented in ACN63103
XX
SQ   Sequence 17 BP; 6 A; 2 C; 8 G; 1 T; 0 U; 0 Other;

  Query Match            17.0%;  Score 3.4;  DB 1;  Length 17;
  Best Local Similarity   80.0%;  Pred. No. 1.3e+02;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          8 AGGCT 12


RESULT 162
ACN72444
ID   ACN72444 standard; DNA; 17 BP.
XX
AC   ACN72444;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Human GDMLP-1 probe SEQ ID NO:9346.
XX
KW   Human; ss; probe; myosin-like protein-1; hGDMLP-1;
KW   hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
KW   skeletal muscle function.
XX
OS   Homo sapiens.
XX
PN   US2004137589-A1.
XX
PD   15-JUL-2004.
XX
PF   26-NOV-2003; 2003US-00723361.
XX
PR   26-MAY-2000; 2000US-0207456P.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
PR   30-JAN-2001; 2001WO-US000661.
PR   30-JAN-2001; 2001WO-US000662.
PR   30-JAN-2001; 2001WO-US000663.
PR   30-JAN-2001; 2001WO-US000664.
PR   30-JAN-2001; 2001WO-US000665.
PR   30-JAN-2001; 2001WO-US000666.
PR   30-JAN-2001; 2001WO-US000667.
PR   30-JAN-2001; 2001WO-US000668.
PR   30-JAN-2001; 2001WO-US000669.
PR   30-JAN-2001; 2001WO-US000670.
PR   05-FEB-2001; 2001US-0266860P.
PR   25-MAY-2001; 2001US-00866108.
XX
PA   (GUYY/) GU Y.
PA   (JIYY/) JI Y.
PA   (PENN/) PENN S G.
PA   (HANZ/) HANZEL D K.
PA   (RANK/) RANK D.
```

PA (CHEN/) CHEN W.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
XX
DR WPI; 2004-533378/51.
XX
PT Novel myosin-like protein-1, useful for treating or preventing disorder
PT associated with decreased expression or activity of human genome-derived
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT function.
XX
PS Disclosure; SEQ ID NO 9346; 0pp; English.
XX
CC The invention relates to a novel polypeptide (I) comprising a sequence
CC (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully
CC defined in the specification, a fragment of at least 8 amino acids of
CC (S1), 95% deviation from (S1) which are conservative substitutions, and
CC 65% identity to (S1). A polypeptide of the invention acts as a agonist or
CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A
CC pharmaceutical composition of the invention is useful for treating or
CC preventing a disorder associated with decreased expression or activity of
CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
CC The present sequence represents a 17-mer nucleotide, used in the
CC invention for scanning the sequence represented in ACN63103
XX
SQ Sequence 17 BP; 5 A; 3 C; 8 G; 1 T; 0 U; 0 Other;

Query Match 17.0%; Score 3.4; DB 1; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 AGTCT 13
|| ||
Db 6 AGGCT 10

RESULT 163
ADP69113/c
ID ADP69113 standard; DNA; 20 BP.
XX
AC ADP69113;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human mitoNEET-specific antisense oligonucleotide #7.
XX
KW human; antisense oligonucleotide; mitochondrial membrane;
KW insulin sensitising antidiabetic thiazolodinediones; mitoNEET; diabetes;
KW immunological disorder; cardiovascular disorder; including hypertension;
KW neurological disorders; ischaemia; reperfusion; ss;
KW 2'-methoxyethyl gapmer; 2'-MOE gapmer; phosphorothioate backbone.
XX
OS Homo sapiens.
XX
PN WO2004053060-A2.
XX
PD 24-JUN-2004.
XX
PF 25-NOV-2003; 2003WO-US037621.
XX
PR 06-DEC-2002; 2002US-0431529P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Colca JR;
XX
DR WPI; 2004-468836/44.
XX
PT New antisense oligonucleotides encoding mitoNEET, useful for modulating
PT mitoNEET expression or for treating diseases associated with mitoNEET,
PT e.g. diabetes, immunological disorders or cardiovascular disorders.
XX
PS Claim 4; SEQ ID NO 7; 226pp; English.
XX
CC The invention comprises antisense oligonucleotides that are targeted to
CC the nucleic acids encoding a family of human proteins from mitochondrial
CC membranes, which bind insulin sensitising, antidiabetic
CC thiazolodinediones (referred to as: mitoNEET). The antisense
CC oligonucleotides of the invention are useful for modulating mitoNEET
CC expression and for treating diseases or conditions associated with
CC mitoNEET, such as: diabetes, immunological disorders, cardiovascular
CC disorders including hypertension, neurological disorders, and
CC ischaemia/reperfusion injuries. The present DNA sequence represents a
CC mitoNEET-specific antisense oligonucleotide of the invention. NOTE: The
CC present sequence is a 2'-methoxyethyl (2'-MOE) gapmer with a
CC phosphorothioate backbone.
XX
SQ Sequence 20 BP; 2 A; 6 C; 3 G; 9 T; 0 U; 0 Other;

Query Match 17.0%; Score 3.4; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 AGTCT 13
|| ||
Db 10 AGACT 6

RESULT 164
ADP69111/c
ID ADP69111 standard; DNA; 20 BP.
XX
AC ADP69111;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human mitoNEET-specific antisense oligonucleotide #5.
XX
KW human; antisense oligonucleotide; mitochondrial membrane;
KW insulin sensitising antidiabetic thiazolodinediones; mitoNEET; diabetes;
KW immunological disorder; cardiovascular disorder; including hypertension;
KW neurological disorders; ischaemia; reperfusion; ss;
KW 2'-methoxyethyl gapmer; 2'-MOE gapmer; phosphorothioate backbone.
XX
OS Homo sapiens.
XX
PN WO2004053060-A2.
XX
PD 24-JUN-2004.
XX
PF 25-NOV-2003; 2003WO-US037621.
XX
PR 06-DEC-2002; 2002US-0431529P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Colca JR;
XX
DR WPI; 2004-468836/44.
XX
PT New antisense oligonucleotides encoding mitoNEET, useful for modulating
PT mitoNEET expression or for treating diseases associated with mitoNEET,
PT e.g. diabetes, immunological disorders or cardiovascular disorders.
XX
PS Claim 4; SEQ ID NO 5; 226pp; English.
XX
CC The invention comprises antisense oligonucleotides that are targeted to
CC the nucleic acids encoding a family of human proteins from mitochondrial
CC membranes, which bind insulin sensitising, antidiabetic
CC thiazolodinediones (referred to as: mitoNEET). The antisense
CC oligonucleotides of the invention are useful for modulating mitoNEET
CC expression and for treating diseases or conditions associated with
CC mitoNEET, such as: diabetes, immunological disorders, cardiovascular
CC disorders including hypertension, neurological disorders, and
CC ischaemia/reperfusion injuries. The present DNA sequence represents a

```
CC   mitoNEET-specific antisense oligonucleotide of the invention. NOTE: The
CC   present sequence is a 2'-methoxyethyl (2'-MOE) gapmer with a
CC   phosphorothioate backbone.
XX
SQ   Sequence 20 BP; 2 A; 6 C; 3 G; 9 T; 0 U; 0 Other;

  Query Match            17.0%;  Score 3.4;  DB 1;  Length 20;
  Best Local Similarity  80.0%;  Pred. No. 1.1e+02;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          9 AGACT 5


RESULT 165
AAT09601/c
ID   AAT09601 standard; DNA; 8 BP.
XX
AC   AAT09601;
XX
DT   25-MAR-2003  (revised)
DT   25-JUN-1996  (first entry)
XX
DE   3'-primer used for characterisation of human biological samples.
XX
KW   3'-primer; human; protein coding region; PCR primer kit;
KW   characterisation; biological samples; PCR amplification; indexing;
KW   identification; cloning; analysis; genes; genome mapping;
KW   disease diagnosis; ss.
XX
OS   Synthetic.
XX
PN   WO9531574-A1.
XX
PD   23-NOV-1995.
XX
PF   12-MAY-1995;   95WO-US006032.
XX
PR   16-MAY-1994;   94US-00242887.
XX
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
PI   Lopeznieto CE,  Nigam SK;
XX
DR   WPI; 1996-010958/01.
XX
PT   Characterisation of nucleotide sequences using primer pairs - by PCR
PT   amplification and indexing of amplification prods. w.r.t. primers used
PT   for genome mapping and disease diagnosis.
XX
PS   Disclosure; Page 19; 72pp; English.
XX
CC   The 5'-primers AAT09358-508, and the 3'-primers AAT09509-659, which
CC   target human protein coding regions, together comprise a PCR primer kit
CC   with 1361 possible primer pairs. The kit is used in a new method for the
CC   characterisation of nucleic acid sequences obtd. from human biological
CC   samples, which comprises PCR amplification and indexing of the prods.
CC   w.r.t the primer pair that hybridised to its delineating subsequences.
CC   The method may be used in the identification, cloning and analysis of
CC   genes, e.g. in genome mapping, and disease diagnosis. (Updated on 25-MAR-
CC   2003 to correct PI field.)
XX
SQ   Sequence 8 BP; 1 A; 3 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match            16.0%;  Score 3.2;  DB 1;  Length 8;
  Best Local Similarity  62.5%;  Pred. No. 2.8e+02;
  Matches    5;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 CTCCAGTC 12
              ||  || |
Db          8 CTGGAGAC 1


RESULT 166
AAT09436
ID   AAT09436 standard; DNA; 8 BP.
XX
AC   AAT09436;
XX
DT   25-MAR-2003  (revised)
DT   21-JUN-1996  (first entry)
XX
DE   5'-primer used for characterisation of human biological samples.
XX
KW   5'-primer; human; protein coding region; PCR primer kit;
KW   characterisation; biological samples; PCR amplification; indexing;
KW   identification; cloning; analysis; genes; genome mapping;
KW   disease diagnosis; ss.
XX
OS   Synthetic.
XX
PN   WO9531574-A1.
XX
PD   23-NOV-1995.
XX
PF   12-MAY-1995;   95WO-US006032.
XX
PR   16-MAY-1994;   94US-00242887.
XX
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
PI   Lopeznieto CE,  Nigam SK;
XX
DR   WPI; 1996-010958/01.
XX
PT   Characterisation of nucleotide sequences using primer pairs - by PCR
PT   amplification and indexing of amplification prods. w.r.t. primers used
PT   for genome mapping and disease diagnosis.
XX
PS   Claim 5; Page 44; 72pp; English.
XX
CC   The 5'-primers AAT09358-508, and the 3'-primers AAT09509-659, which
CC   target human protein coding regions, together comprise a PCR primer kit
CC   with 1361 possible primer pairs. The kit is used in a new method for the
CC   characterisation of nucleic acid sequences obtd. from human biological
CC   samples, which comprises PCR amplification and indexing of the prods.
CC   w.r.t the primer pair that hybridised to its delineating subsequences.
CC   The method may be used in the identification, cloning and analysis of
CC   genes, e.g. in genome mapping, and disease diagnosis. (Updated on 25-MAR-
CC   2003 to correct PI field.)
XX
SQ   Sequence 8 BP; 2 A; 2 C; 3 G; 1 T; 0 U; 0 Other;

  Query Match            16.0%;  Score 3.2;  DB 1;  Length 8;
  Best Local Similarity  62.5%;  Pred. No. 2.8e+02;
  Matches    5;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 CTCCAGTC 12
              ||  || |
Db          1 CTGGAGAC 8


RESULT 167
AAZ78224
ID   AAZ78224 standard; DNA; 10 BP.
XX
AC   AAZ78224;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:652.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
```

KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS Homo sapiens.
XX
PN WO9965924-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013800.
XX
PR 19-JUN-1998; 98US-0089833P.
PR 19-JUN-1998; 98US-0089844P.
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089878P.
PR 19-JUN-1998; 98US-0089991P.
PR 19-JUN-1998; 98US-0089992P.
PR 19-JUN-1998; 98US-0089993P.
PR 19-JUN-1998; 98US-0089994P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0089999P.
PR 19-JUN-1998; 98US-0090000P.
PR 19-JUN-1998; 98US-0090035P.
PR 19-JUN-1998; 98US-0090036P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
PR 19-JUN-1998; 98US-0090042P.
PR 19-JUN-1998; 98US-0090043P.
PR 19-JUN-1998; 98US-0090044P.
PR 19-JUN-1998; 98US-0090045P.
PR 19-JUN-1998; 98US-0090047P.
PR 19-JUN-1998; 98US-0090048P.
PR 19-JUN-1998; 98US-0090072P.
PR 19-JUN-1998; 98US-0090076P.
PR 19-JUN-1998; 98US-0090077P.
PR 19-JUN-1998; 98US-0090078P.
PR 19-JUN-1998; 98US-0090079P.
PR 19-JUN-1998; 98US-0090080P.
PR 08-DEC-1998; 98US-0111715P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106077/09.
XX
PT Isolated polynucleotides differentially expressed in antigen-presenting
PT cells, useful in gene vaccines against cancer.
XX
PS Claim 1; Page 84; 130pp; English.
XX
CC Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC expression) tags used to identify mRNA transcripts encoding
CC immunostimulatory cofactor proteins which are preferentially or
CC differentially expressed in monocyte-derived dendritic cells compared
CC with monocytes. Some of the transcripts correspond to known genes or ESTs
CC (expressed sequence tags) which were previously unknown to be
CC preferentially or differentially expressed in dendritic cells, while
CC other transcripts correspond to novel genes. Antigen-presenting cell
CC (APC)-associated costimulatory factors play an important role in the
CC activation of the cytotoxic immune response, particularly against tumour
CC cells. Tumour antigen presentation via the MHC (major histocompatibility
CC complex) and subsequent recognition by T-cell receptors is alone
CC insufficient to activate a robust cytotoxic immune response that can lyse
CC the tumour cells, immunostimulatory cofactors also being required for
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC sequences identified using the SAGE tags have several potential uses.
CC They may be used in vaccines to induce an immune response, particularly
CC against a tumour antigen; to modulate the genotype of an APC; to screen
CC for agents that modulate expression of differentially expressed genes in
CC an APC; and as hybridisation probes/amplification primers for the
CC diagnosis, prognosis and monitoring of diseases related to abnormal
CC expression of these genes. Detection of the dendritic cell differentially
CC expressed genes, or of their encoded proteins, can be used to identify
CC cells as belonging to the monocyte lineage. Cells containing these genes
CC can be used in active immunotherapy (or to stimulate production of a
CC population of antigen-specific effector cells) and vectors containing
CC them are used in gene therapy. Co-administration of tumour antigens and
CC APC-associated costimulatory factors ensures adequate antigen
CC presentation to endogenous APCs and upregulates the APCs for the
CC presentation of co-stimulatory signals, migration to T cell-rich sites,
CC secretion of T cell growth factors and secretion of chemokines for
CC recruitment of immune effector cells
XX
SQ Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 16.0%; Score 3.2; DB 1; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CTCCAGTC 12
|| || |
Db 2 CTGGAGCC 9

RESULT 168
AAZ80874
ID AAZ80874 standard; DNA; 10 BP.
XX
AC AAZ80874;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #108.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 61; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and

CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effecter
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 16.0%; Score 3.2; DB 1; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CTCCAGTC 12
|| || |
Db 3 CTGGAGAC 10

RESULT 169
AAS95346/c
ID AAS95346 standard; DNA; 10 BP.
XX
AC AAS95346;
XX
DT 14-FEB-2002 (first entry)
XX
DE Human Histamine H2 receptor ASO primer extension PCR primer #6.
XX
KW Human; histamine H2 receptor; HRH2; ss; PCR primer; polymorphic variant;
KW haplotyping; genotyping; acid-peptic disorder; mammary cancer;
KW gastric carcinoma; allele specific oligonucleotide; ASO;
KW primer extension.
XX
OS Homo sapiens.
XX
PN WO200179220-A2.
XX
PD 25-OCT-2001.
XX
PF 12-APR-2001; 2001WO-US011941.
XX
PR 12-APR-2000; 2000US-0196406P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Chew A, Choi JY, Koshy B;
XX
DR WPI; 2002-055249/07.
XX
PT New human histamine H2 receptor (HRH2) isogene polymorphic variants,
PT useful in expressing HRH2 protein for use in screening for candidate
PT drugs to treat diseases related to HRH2 activity.
XX
PS Claim 17; Page 14; 62pp; English.
XX
CC The invention relates to an isolated polynucleotide comprising a
CC polymorphic variant of a reference sequence for human Histamine H2
CC receptor (HRH2) gene, its fragment or complement, and the polymorphic
CC variant contains an HRH2 isogene defined by a haplotype listed in the
CC specification. Also disclosed are methods for haplotyping and genotyping
CC the HRH2 gene of an individual, a method for predicting a haplotype pair
CC for the HRH2 gene of an individual, identifying an association between a
CC trait and at least one haplotype or haplotype pair of HRH2 gene, allele
CC specific oligonucleotides (ASO) for performing the haplotyping/
CC genotyping, a recombinant nonhuman organisms transformed or transfected
CC with the polymorphic variant, the protein expressed by the polymorphic
CC variant, an antibody raised against the protein and screening for drugs
CC targeting the polypeptide by contacting HRH2 polymorphic variant with a
CC candidate agent and assaying for binding activity. The polymorphisms are
CC useful for studying the biological function of HRH2 gene, as well as in
CC identifying drugs targeting this protein for the treatment of disorder
CC related to its abnormal expression or function. The polymorphic variants
CC may be used in screening for compounds targeting CALM1 to treat a
CC specific condition or disease predicted to be associated with HRH2
CC activity, in studying the effect of the variation on the biological
CC activity of HRH2 as well as on the binding affinity of candidate drugs
CC targeting HRH2 for the treatment of acid-peptic disorders of the
CC gastrointestinal tract and also possibly human mammary cancer and gastric
CC carcinoma. The polymorphism and haplotype data can also be used for
CC validating whether HRH2 is a suitable drug target for drugs to treat acid
CC -peptic disorders of the gastrointestinal tract, screening of such drugs
CC and reducing bias in clinical trials of such drugs. The present sequence
CC is the 3' terminus of an ASO primer extension PCR primer used to detect
CC the polymorphisms of the invention
XX
SQ Sequence 10 BP; 1 A; 5 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 16.0%; Score 3.2; DB 1; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GTCTCCAG 10
| || ||
Db 8 GACTGGAG 1

RESULT 170
ABV70379
ID ABV70379 standard; cDNA; 11 BP.
XX
AC ABV70379;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 8165.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Claim 24; Page 261; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or

```
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 3 A; 4 C; 3 G; 1 T; 0 U; 0 Other;

  Query Match            16.0%;  Score 3.2;  DB 1;  Length 11;
  Best Local Similarity  62.5%;  Pred. No. 1.6e+02;
  Matches    5;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 CTCCAGTC 12
              ||  || |
Db          3 CTGGAGAC 10


RESULT 171
ABV62958
ID   ABV62958 standard; cDNA; 11 BP.
XX
AC   ABV62958;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 744.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 45; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 3 A; 4 C; 3 G; 1 T; 0 U; 0 Other;

  Query Match            16.0%;  Score 3.2;  DB 1;  Length 11;
  Best Local Similarity  62.5%;  Pred. No. 1.6e+02;
  Matches    5;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 CTCCAGTC 12
              ||  || |
Db          3 CTGGAGAC 10


RESULT 172
AAV05484/c
ID   AAV05484 standard; DNA; 10 BP.
XX
AC   AAV05484;
XX
DT   01-MAY-1998  (first entry)
XX
DE   BsmAI restriction recognition site.
XX
KW   Amplification; nucleic acid sequence; SDA; recognition site;
KW   strand displacement amplification; restriction endonuclease;
KW   alpha-boronated deoxynucleoside triphosphate; BsaI;
KW   hemimodified restriction site; ds.
XX
OS   Synthetic.
XX
PN   US5702926-A.
XX
PD   30-DEC-1997.
XX
PF   22-AUG-1996;   96US-00701270.
XX
PR   22-AUG-1996;   96US-00701270.
XX
PA   (BECT ) BECTON DICKINSON CO.
XX
PI   Walker GT,  Fraiser MS;
XX
DR   WPI; 1998-076416/07.
XX
PT   Strand displacement amplification of nucleic acids - using alpha-
PT   boronated deoxy:nucleoside tri:phosphate to create nickable restriction
PT   site.
XX
PS   Disclosure; Col 6; 7pp; English.
XX
CC   A novel method for amplifying a target nucleic acid sequence by strand
CC   displacement amplification (SDA) comprises, amplifying the target
CC   sequence in an SDA reaction in which an alpha-boronated deoxynucleoside
CC   triphosphate is incorporated into a double stranded recognition site for
CC   a restriction endonuclease, e.g. the present sequence. This produces a
CC   hemimodified restriction site that is nicked by the restriction
CC   endonuclease during the SDA reaction. Most alpha-boronated dNTP will
CC   mimic a corresponding alpha-thiolated dNTP in essentially all respects as
CC   regards SDA, though amplification efficiency is reduced in SDA reactions
CC   optimised for alpha-thiolated dNTP
XX
SQ   Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match            15.0%;  Score 3;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 1.6e+02;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTG 3
              |||
Db          8 TTG 6


RESULT 173
AAF41789
ID   AAF41789 standard; DNA; 10 BP.
XX
AC   AAF41789;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8528.
```

XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 304; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 4 A; 0 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 15.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AGT 11
|||
Db 7 AGT 9

RESULT 174
AAF69645
ID AAF69645 standard; DNA; 10 BP.
XX
AC AAF69645;
XX
DT 18-APR-2001 (first entry)
XX
DE Human IL4Ralpha gene probe #285.
XX
KW Polymorphism; human; interleukin 4 receptor-alpha; IL4R-alpha;
KW allergic disease; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200104270-A1.
XX
PD 18-JAN-2001.
XX
PF 13-JUL-2000; 2000WO-US019094.
XX
PR 13-JUL-1999; 99US-0143435P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Chew A, Denton RR, Duda A, Nandabalan K, Stephens JC;
PI Windemuth AK;
XX
DR WPI; 2001-103078/11.
XX
PT New isolated polynucleotide useful for the identification of therapeutics
PT in allergic diseases is new.
XX
PS Disclosure; Page 46; 188pp; English.
XX
CC The present invention relates to polymorphisms of the human interleukin 4
CC receptor-alpha gene (IL4R-alpha; see AAF57718 for the reference
CC sequence). Polynucleotides comprising polymorphic gene variants are
CC useful for therapeutic purposes. For example, where a patient may benefit
CC from expression of a particular IL4Ralpha protein isoform, an expression
CC vector encoding the isoform may be administered to the patient. It may
CC desirable to decrease or block expression of a particular IL4Ralpha
CC isogene, which may be done by turning off by transforming a targeted
CC organ, tissue or cell population with an expression vector that expresses
CC high levels of untranslatable mRNA for the isogene. Specific therapeutics
CC identified by these methods may be useful for allergic diseases. The
CC present sequence is a probe for human IL4R-alpha
XX
SQ Sequence 10 BP; 3 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 15.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CAG 10
|||
Db 7 CAG 9

RESULT 175
AAA81188
ID AAA81188 standard; DNA; 8 BP.
XX
AC AAA81188;
XX
DT 24-NOV-2000 (first entry)
XX
DE A. thaliana primer walking octamer SEQ ID NO: 501.
XX
KW Primer walking; octamer; primer; DNA sequencing; PCR; ss.
XX
OS Arabidopsis thaliana.
XX
PN US6083695-A.
XX
PD 04-JUL-2000.
XX
PF 21-MAY-1997; 97US-00859954.
XX

PR 15-APR-1996; 96US-00632782.
XX
PA (UYHO-) UNIV HOUSTON.
PA (HARD/) HARDIN S H.
XX
PI Hardin PE, Hardin SH, Homayouni R;
XX
DR WPI; 2000-474852/41.
XX
PT Sequencing an unknown DNA molecule for the polymerase chain reaction and
PT other primer processes comprises primer walking of octamer
PT oligonucleotides.
XX
PS Claim 1; Col 277-278; 161pp; English.
XX
CC This invention describes a novel method for sequencing an unknown DNA
CC molecule which comprises selecting a library primer from an octamer
CC oligonucleotide library consisting of 48 8-bp sequences and corresponding
CC complementary sequences, where the library primer is complementary to a
CC known sequence adjacent to the unknown sequence or is complementary to a
CC sequence in a known extension product. The method is useful for DNA
CC nucleotide sequencing, in PCR, and in other processes which make use of
CC primers. The octamers are used to identify coding sequences. Primer
CC walking using the octamer libraries is advantageous over other sequencing
CC methods because it does not require multiple cloning steps nor subsequent
CC template preparations, and it is a directed and methodical approach.
CC AAA80688-A81253 represent the octamer primers used in the primer walking
CC method of the invention
XX
SQ Sequence 8 BP; 3 A; 1 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 14.0%; Score 2.8; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CTCCAG 10
|| ||
Db 2 CTGGAG 7

RESULT 176
ADH69419/c
ID ADH69419 standard; DNA; 10 BP.
XX
AC ADH69419;
XX
DT 25-MAR-2004 (first entry)
XX
DE Exon 4/5 junction #2of Blue pigment gene.
XX
KW Human; Blue pigment gene; retina specific gene; ds; cancer; infection;
KW cytostatic; GAWTS; genomic amplification with transcript sequencing;
KW RAWTS; RNA amplification with transcript sequencing; tsRAWTS;
KW tissue specific RAWTS; RAWIT;
KW RNA amplification with in vitro translation; zooRAWTS; ASAWTS;
KW adjacent sequence amplification with transcript sequencing; PASA;
KW PCR amplification of specific alleles; PLATS;
KW promoter ligation with transcript sequencing.
XX
OS Homo sapiens.
XX
PN US2003143553-A1.
XX
PD 31-JUL-2003.
XX
PF 07-MAR-2002; 2002US-00094507.
XX
PR 28-JAN-1988; 88US-00149312.
PR 24-JUL-1989; 89US-00385013.
PR 12-NOV-1993; 93US-00151461.
PR 27-DEC-1994; 94US-00399855.
PR 22-FEB-2000; 2000US-00510177.
XX
PA (SOMM/) SOMMER S S.
XX
PI Sommer SS;
XX
DR WPI; 2003-730802/69.
XX
PT Amplifying a sequence of interest present within a nucleic acid molecule
PT for monitoring the progression of cancer by obtaining a sample of the
PT nucleic acid molecule and contacting the sample with an RNA polymerase.
XX
PS Disclosure; Fig 1B; 70pp; English.
XX
CC The invention relates to amplifying a sequence of interest present within
CC a nucleic acid molecule comprising: obtaining a sample of the nucleic
CC acid molecule that contains the sequence of interest; if the nucleic acid
CC is a single-stranded RNA molecule, treating the sample so as to prepare a
CC sample containing DNA molecule that contains a sequence complementary to
CC the sequence of interest; treating the sample to obtain a further sample;
CC contacting the further sample under hybridisation conditions with one
CC oligonucleotide primer that includes at least a promoter and a nucleic
CC acid present within the nucleic acid molecule, where the primer sequence
CC is located adjacent to, and 5' of, the sequence of interest, so that the
CC oligonucleotide primer hybridises with the single-stranded DNA molecule;
CC treating the resulting sample containing the single stranded DNA molecule
CC to which the oligonucleotide primer is hybridised from step (4) with a
CC polymerase under polymerizing conditions so that a DNA extension product
CC of the oligonucleotide primer is synthesised and contains the sequence of
CC interest; treating the sample from step (5) so as to separate the DNA
CC extension product from the single-stranded DNA molecule on which it was
CC synthesised; contacting the resulting sample from step (6) containing the
CC sequence complementary to the sequence of interest under hybridisation
CC conditions, with one oligonucleotide primer; treating the sample
CC containing the single-stranded DNA molecule to which the oligonucleotide
CC primer is hybridised from step (7) with a polymerase so as to synthesise
CC a further DNA extension product; repeating steps (7)-(9), as desired;
CC contacting the sample from step (10) with an RNA polymerase that
CC initiates polymerization from the promoter present, under polymerising
CC conditions, so as to obtain multiple RNA transcripts of each DNA
CC extension product that contains the sequence complementary to the
CC sequence of interest. The promoter is a phage promoter, which is T7, T3
CC or SP6 promoter. The method (and its modifications detailed in the
CC specification are known as GAWTS (genomic amplification with transcript
CC sequencing), RAWTS (RNA amplification with transcript sequencing),
CC tsRAWTS (tissue specific RAWTS), RAWIT (RNA amplification with in vitro
CC translation), zooRAWTS (sequencing homologous genes across species)
CC ASAWTS (adjacent sequence amplification with transcript sequencing), PASA
CC (PCR amplification of specific alleles) and PLATS (promoter ligation with
CC transcript sequencing). The method is useful for amplifying a sequence of
CC interest present within a nucleic acid molecule for monitoring the
CC progression of cancer or the efficiency of treatment of cancer or for
CC diagnosing and subtyping infectious agents. The present sequence is a
CC human retina specific blue pigment gene exon 4/5 junction sequence
CC analysed by the method of the invention.
XX
SQ Sequence 10 BP; 1 A; 4 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 14.0%; Score 2.8; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CTCCAG 10
|| ||
Db 10 CTGGAG 5

RESULT 177
AAV50258/c
ID AAV50258 standard; DNA; 10 BP.
XX
AC AAV50258;
XX
DT 21-OCT-1998 (first entry)
XX

```
DE   Yeast tag for additional NORF chromosome 4 tag position 381712.
XX
KW   Yeast; Saccharomyces cerevisiae; transcriptome; cell cycle; regulation;
KW   eukaryotic cell; antifungal; SAGE tag; gene expression;
KW   serial analysis of gene expression; probe; ss.
XX
OS   Saccharomyces cerevisiae.
OS   Synthetic.
XX
PN   WO9832847-A2.
XX
PD   30-JUL-1998.
XX
PF   22-JAN-1998;   98WO-US001216.
XX
PR   23-JAN-1997;   97US-0035917P.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 1998-427943/36.
XX
PT   Yeast transcriptome - useful for modulating eukaryotic cell, for
PT   screening antifungal agents, and for identifying genes in cell cycle
PT   progression.
XX
PS   Claim 1; Page 26; 44pp; English.
XX
CC   Yeast transcriptome is encoded by a DNA molecule comprising a yeast gene
CC   involved in cell cycle progression selected from the group of
CC   nonannotated ORF (NORF) genes. SAGE (serial analysis gene expression)
CC   tags for highly expressed genes and NORF genes are given in AAV50051 to
CC   AAV50345. The present invention describes: (1) a method of using yeast
CC   genes to modulate the cell cycle which comprises administering to a cell
CC   an isolated DNA molecule comprising a yeast gene which is involved in
CC   cell cycle progression selected from differentially expressed genes (SAGE
CC   tags given in AAV50051 to AAV50345); (2) a method for screening candidate
CC   antifungal drugs which comprises contacting a test substance with a yeast
CC   cell and monitoring expression of a yeast gene which is involved in cell
CC   cycle progression; (3) a method of identifying human genes which are
CC   involved in cell cycle progression which comprises hybridizing a probe
CC   comprising at least 10 contiguous nucleotides of a yeast gene which is
CC   differentially expressed between at least 2 phases selected from the log
CC   phase, the S phase and the G2/M phase; and (4) a probe for ascertaining
CC   the phase in the cell cycle, where the probe comprises at least 14
CC   contiguous nucleotides of a NORF gene (SAGE tags given in AAV50051 to
CC   AAV50345), or as an array of probes on a solid support
XX
SQ   Sequence 10 BP; 1 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             14.0%;  Score 2.8;  DB 1;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 1.7e+02;
  Matches    4;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CTCCAG 10
              ||  ||
Db          7 CTGGAG 2


RESULT 178
AAZ83592
ID   AAZ83592 standard; DNA; 10 BP.
XX
AC   AAZ83592;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #2826.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 134; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 4 A; 1 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             14.0%;  Score 2.8;  DB 1;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 1.7e+02;
  Matches    4;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CTCCAG 10
              ||  ||
Db          4 CTGGAG 9


RESULT 179
AAZ85035/c
ID   AAZ85035 standard; DNA; 10 BP.
XX
AC   AAZ85035;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #4269.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
```

KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 173; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effecter
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 2 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 14.0%; Score 2.8; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CTCCAG 10
|| ||
Db 9 CTGGAG 4

RESULT 180
AAC74005/c
ID AAC74005 standard; cDNA; 10 BP.
XX
AC AAC74005;
XX
DT 02-FEB-2001 (first entry)
XX
DE Human dendritic cell cDNA base sequence oligonucleotide #92.
XX
KW Human; dendritic cell; monocyte; immune system; diagnosis; cancer;
KW autoimmune disease; tumour; ss.
XX
OS Homo sapiens.
XX
PN WO200060074-A1.
XX
PD 12-OCT-2000.
XX
PF 30-MAR-2000; 2000WO-JP002019.
XX
PR 01-APR-1999; 99JP-00095481.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Hashimoto S, Matsushima K, Suzuki T;
XX
DR WPI; 2000-619172/59.
XX
PT Groups of genes expressed in human dendritic cells at a greater or lesser
PT extent than in monocytes for investigation and diagnosis of autoimmune
PT disease and tumors.
XX
PS Claim 1; Page 10; 95pp; Japanese.
XX
CC The present invention describes a group of genes consisting of 100 genes
CC which are highly expressed in human dendritic cells; a group of genes
CC which are expressed at a higher frequency in human dendritic cells than
CC in human monocytes; and a group of genes which are expressed at lower
CC frequency in human dendritic cells than in human monocytes. Each group of
CC genes are characterised in that cDNAs of these genes respectively have
CC the base sequences of SEQ ID NO:1 to 100 (AAC73914 to AAC74013), SEQ ID
CC NO:101 to 200 (AAC74014 to AAC74113) and SEQ ID NO:201 to 300 (AAC74114
CC to AAC74213), each is continuous with the base sequence 5'-CATG-3'
CC located most closely to the poly-A region. The sequences can be used for
CC the investigation of the role and mechanism of the involvement of
CC dendritic cells in the immune system and for the study and diagnosis of
CC diseases in which dendritic cells play a significant role, e.g. cancers
CC and autoimmune diseases
XX
SQ Sequence 10 BP; 2 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 14.0%; Score 2.8; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CTCCAG 10
|| ||
Db 9 CTGGAG 4

RESULT 181
AAA56168/c
ID AAA56168 standard; DNA; 10 BP.
XX
AC AAA56168;
XX
DT 07-SEP-2000 (first entry)
XX
DE Human monocyte gene Tag oligonucleotide sequence SEQ ID NO:62.
XX
KW Human; monocyte; macrophage; GM-macrophage; M-macrophage; tag;
KW granulocyte-macrophage colony-stimulating factor; characterisation;
KW GM-CSF; identification; diagnosis; gene specificity; oncogenesis;
KW disease onset mechanism; genetic disease; drug development; ss.
XX
OS Homo sapiens.
XX
PN WO200024892-A1.
XX
PD 04-MAY-2000.
XX

PF 28-OCT-1999; 99WO-JP005982.
XX
PR 28-OCT-1998; 98JP-00307532.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Hashimoto S, Matsushima K, Suzuki T;
XX
DR WPI; 2000-350734/30.
XX
PT Genes most frequently expressed in human monocytes and GM-macrophages and
PT M-macrophages studied and with cDNAs characterized, for study of gene
PT specificity, disease onset mechanism, drug development and diagnosis.
XX
PS Claim 1; Page 51; 138pp; Japanese.
XX
CC The present invention describes 100 human genes, which are expressed most
CC frequently in human monocytes. The cDNA of each gene has a sequence fully
CC defined in the specification, and lacking the CATG sequence located
CC adjacent to polyA region. Also described are: (1) an antibody
CC specifically for the protein encoded by any of the genes; (2)
CC oligonucleotides obtained from the cDNA sequences; (3) 380 human genes
CC which are expressed most frequently in human macrophages, differentiated
CC from human monocytes by granulocyte-macrophage colony-stimulating factor,
CC the cDNA of each gene has a fully defined sequence, given in the
CC specification, lacking the base sequence CATG located most closely to the
CC poly A region; (4) an antibody specifically for the protein encoded by
CC any of the genes of (3); and (5) oligonucleotides obtained from the cDNA
CC sequences of (3). The genes and cDNAs, are used for the study of gene
CC specificity and disease onset mechanism e.g. oncogenesis, genetic
CC diseases, drug development and diagnosis. AAA56107 to AAA56586 represent
CC specifically claimed oligonucleotide tag sequences for human genes
CC expressed in monocytes and macrophages
XX
SQ Sequence 10 BP; 2 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

```
  Query Match             14.0%;  Score 2.8;  DB 1;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 1.7e+02;
  Matches    4;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CTCCAG 10
              ||  ||
Db          9 CTGGAG 4
```

RESULT 182
AAH63530/c
ID AAH63530 standard; cDNA; 10 BP.
XX
AC AAH63530;
XX
DT 20-SEP-2001 (first entry)
XX
DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 370.
XX
KW Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX
OS Homo sapiens.
XX
PN WO200138577-A2.
XX
PD 31-MAY-2001.
XX
PF 21-NOV-2000; 2000WO-US031922.
XX
PR 24-NOV-1999; 99US-00448480.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu VE, Vogelstein B, Kinzler KW;
XX
DR WPI; 2001-367706/38.
XX
PT New isolated polynucleotides, useful for identifying specific cell type,
PT such as cancer cell, comprises transcriptomes expressed in particular
PT cell types.
XX
PS Claim 13; Page 47; 94pp; English.
XX
CC The present invention describes a method of identifying the type of cell
CC in a sample, involving determining which of the sequences AAH63161-
CC AAH64724 is expressed by the cell. The transcriptomes described in the
CC invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of the
CC transcriptomes described in the exemplification of the invention
XX
SQ Sequence 10 BP; 2 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

```
  Query Match             14.0%;  Score 2.8;  DB 1;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 1.7e+02;
  Matches    4;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CTCCAG 10
              ||  ||
Db          9 CTGGAG 4
```

RESULT 183
AAF38187/c
ID AAF38187 standard; DNA; 10 BP.
XX
AC AAF38187;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4926.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 175; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast

CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 1 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 14.0%; Score 2.8; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CTCCAG 10
|| ||
Db 7 CTGGAG 2

RESULT 184
AAF39032/c
ID AAF39032 standard; DNA; 10 BP.
XX
AC AAF39032;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5771.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 206; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 3 A; 3 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 14.0%; Score 2.8; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CTCCAG 10
|| ||
Db 9 CTGGAG 4

RESULT 185
AAF33475/c
ID AAF33475 standard; DNA; 10 BP.
XX
AC AAF33475;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:214.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Claim 1; Page 26; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes

```
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 1 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             14.0%;  Score 2.8;  DB 1;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 1.7e+02;
  Matches    4;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CTCCAG 10
              ||  ||
Db          7 CTGGAG 2


RESULT 186
ABL60204/c
ID   ABL60204 standard; DNA; 10 BP.
XX
AC   ABL60204;
XX
DT   22-JUL-2002  (first entry)
XX
DE   Human MUC1 PCR primer SEQ ID NO 48.
XX
KW   Human; mucin 1; MUC1; transmembrane protein; SNP; cancer; cytostatic;
KW   single nucleotide polymorphism; haplotyping; genotyping; drug;
KW   antiinflammatory; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200226765-A2.
XX
PD   04-APR-2002.
XX
PF   25-SEP-2001; 2001WO-US030151.
XX
PR   28-SEP-2000; 2000US-0236113P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Chew A,  Koshy B;
XX
DR   WPI; 2002-405042/43.
XX
PT   New genetic variants of mucin 1, Transmembrane gene, useful in studying
PT   expression and function of protein encoded by the gene and for screening
PT   drugs to treat diseases e.g. cancer.
XX
PS   Claim 16; Page 14; 75pp; English.
XX
CC   The invention relates to a polynucleotide (ABL60158, ABL60159) encoding
CC   mucin 1/MUC1 (ABB77476), Transmembrane isogene. The invention describes
CC   novel genetic variants of the MUC1 gene. The invention is useful for
CC   haplotyping/genotyping the MUC1 gene in an individual and identifying an
CC   association between a trait and at least one of the haplotypes or
CC   haplotype pairs of MUC1 gene. MUC1 is useful for studying the expression
CC   and function of MUC1 and expressing MUC1 protein for use in screening for
CC   candidate drugs to treat diseases related to MUC1 activity and in
CC   studying the effect of the variation on the biological activity of MUC1
CC   as well as on the binding affinity of candidate drugs targeting MUC1 for
CC   the treatment of e.g. cancer. MUC1 is further used by the pharmaceutical
CC   research scientist to validate MUC1 as a candidate target for and in
CC   design of clinical trials of candidate drugs for, treating a specific
CC   condition drugs or disease predicted to be associated with MUC1 activity.
CC   MUC1 antibodies are useful in a variety of diagnostic and prognostic
CC   formats and therapeutic methods. The present sequence is that of a PCR
CC   primer for detecting MUC1 polymorphisms, useful to the invention
XX
SQ   Sequence 10 BP; 1 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             14.0%;  Score 2.8;  DB 1;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 1.7e+02;
  Matches    4;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          9 AGTCTC 14
              || | |
Db          7 AGACAC 2


RESULT 187
ABV78336/c
ID   ABV78336 standard; cDNA; 10 BP.
XX
AC   ABV78336;
XX
DT   29-NOV-2002  (first entry)
XX
DE   Human ribosomal protein L23 SAGE tag, SEQ ID NO:47.
XX
KW   SAGE tag; serial analysis of gene expression; human; Th1 cell;
KW   activated T cell; T lymphocyte; immune response; expression pattern;
KW   immune disorder; ss.
XX
OS   Homo sapiens.
XX
PN   JP2002186482-A.
XX
PD   02-JUL-2002.
XX
PF   19-DEC-2000; 2000JP-00385816.
XX
PR   19-DEC-2000; 2000JP-00385816.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2002-594261/64.
XX
PT   Human activated Th1 and Th2 cell expression gene group, useful for the
PT   diagnosis and treatment of Th1 and Th2-related diseases.
XX
PS   Claim 1; Page 8; 60pp; Japanese.
XX
CC   The invention relates to SAGE (serial analysis of gene expression) tags
CC   representing groups of genes which are expressed in activated human Th1
CC   and/or Th2 cells. The SAGE tags of this invention consist of a sequence
CC   of 10 nucleotides located downstream of the 5'-CATG-3' sequence motif
CC   lying nearest to the polyA region of cDNAs derived from a variety of
CC   genes. These tags serve to uniquely identify each transcript and can thus
CC   be used to analyse the pattern of gene expression in particular cell
CC   types. The invention also relates to proteins encoded by the genes
CC   expressed in Th1 and/or Th2 cells, antibodies against these proteins, and
CC   inhibitors of the expression of groups of genes that are expressed in
CC   either or both the two cell types. Groups of genes expressed in Th1
CC   and/or Th2 cell types may be used for the diagnosis and treatment of Th1
```

```
CC   and Th2-related disorders. Sequences ABV78290-ABV78339 are SAGE tags
CC   representing 50 genes which are most highly expressed in Th1 cells
XX
SQ   Sequence 10 BP; 2 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             14.0%;  Score 2.8;  DB 1;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 1.7e+02;
  Matches    4;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CTCCAG 10
              ||  ||
Db          9 CTGGAG 4


RESULT 188
ABK23747/c
ID   ABK23747 standard; DNA; 10 BP.
XX
AC   ABK23747;
XX
DT   09-APR-2002  (first entry)
XX
DE   Transcript tag DNA sequence #336 induced or suppressed by N-myc.
XX
KW   Myc-dependent downstream gene; neoplastic; cancer; growth; invasion;
KW   spread; myc target; myc tag; SAGE; serial analysis of gene expression;
KW   myc oncogene; N-myc; human neuroblastoma; cytostatic; ds.
XX
OS   Homo sapiens.
XX
PN   WO200185941-A2.
XX
PD   15-NOV-2001.
XX
PF   11-MAY-2001; 2001WO-NL000361.
XX
PR   11-MAY-2000; 2000EP-00201698.
PR   29-JUN-2000; 2000EP-00202284.
XX
PA   (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.
XX
PI   Versteeg R,  Caron HN;
XX
DR   WPI; 2002-066603/09.
XX
PT   A new nucleic acid library of myc-dependent downstream genes capable of
PT   supporting a neoplastic characteristic of cancer is useful to find new
PT   therapies and diagnoses for cancer.
XX
PS   Disclosure; Page 58; 69pp; English.
XX
CC   The present invention relates to a nucleic acid library comprising myc-
CC   dependent downstream genes or their functional fragments essentially
CC   capable of supporting a neoplastic character of cancer such as growth,
CC   invasion or spread. These myc target or tag sequences are identified by
CC   SAGE (serial analysis of gene expression). The library is useful to find
CC   new diagnoses and treatments for cancer. The invention is also useful to
CC   enhance production of recombinant proteins in a production system with
CC   high expression of endogenous or transfected myc oncogenes. ABK23412-
CC   ABK23828 represent transcript tag DNA sequences that are activated or
CC   repressed by N-myc in human neuroblastoma
XX
SQ   Sequence 10 BP; 2 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             14.0%;  Score 2.8;  DB 1;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 1.7e+02;
  Matches    4;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CTCCAG 10
              ||  ||
Db          9 CTGGAG 4


RESULT 189
ACA94446/c
ID   ACA94446 standard; DNA; 10 BP.
XX
AC   ACA94446;
XX
DT   18-JUL-2003  (first entry)
XX
DE   DNA tag from human transcript elevated in adenomas/cancers #27.
XX
KW   Colorectal cancer; colorectal adenoma; ss; human; renal dipeptidase;
KW   macrophage inhibitory cytokine; MIC; RDP; faeces; blood;
KW   kidney proximal tubule.
XX
OS   Homo sapiens.
XX
PN   WO2003022863-A1.
XX
PD   20-MAR-2003.
XX
PF   09-SEP-2002; 2002WO-US028518.
XX
PR   07-SEP-2001; 2001US-0317494P.
PR   30-MAY-2002; 2002US-0383805P.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI   Buckhaults P,  Kinzler KW,  Vogelstein B;
XX
DR   WPI; 2003-313220/30.
XX
PT   Detecting colorectal cancer in a subject, involves detecting macrophage
PT   inhibitory cytokine or renal dipeptidase or their mRNA in feces or blood
PT   of the subject.
XX
PS   Disclosure; Page 25; 59pp; English.
XX
CC   The invention relates to detecting CC (colorectal cancer e.g. colorectal
CC   adenoma), comprising: (a) detecting macrophage inhibitory cytokine (MIC)
CC   or renal dipeptidase (RDP) in faeces or blood of a subject and comparing
CC   amount of MIC or RDP detected to that in normal subjects, where an
CC   elevated amount of MIC or RDP in the subject is an indicator of CC in
CC   subject; (b) isolating mRNA sample from faeces of a subject, detecting
CC   MIC or RDP mRNA in the mRNA sample, and comparing amount of MIC or RDP
CC   mRNA detected to that in normal subjects, where an elevated amount of MIC
CC   or RDP mRNA in the subject is an indicator of CC in subject; (c)
CC   isolating epithelial cells from blood of a subject, isolating an mRNA
CC   sample from faeces of a subject or epithelial cells, detecting MIC or RDP
CC   mRNA in the mRNA sample, and comparing the amount of MIC or RDP mRNA in
CC   the mRNA sample to amounts of MIC or RDP mRNA in normal subjects, where
CC   an elevated amount of MIC or RDP mRNA in the mRNA sample is an indicative
CC   of CC in the subject; (d) contacting blood or faeces of a subject, with
CC   an RDP substrate, detecting activity of RDP in the blood or faeces by
CC   detection of increased reaction product or decreased RDP substrate, and
CC   comparing the amount of activity of RDP in blood or faeces of the subject
CC   to that in normal subjects, where an elevated amount of activity of RDP
CC   in the blood or faeces of the subject is an indicator of CC in the
CC   subject; (e) administering to a subject an antibody which specifically
CC   binds to RDP or an inhibitor of RDP, where the antibody or inhibitor is
CC   labeled with a moiety which is detectable from outside of the subject and
CC   detecting the moiety in the subject from outside of the subject, where an
CC   area of localisation of the moiety within the subject but outside the
CC   proximal tubules of the kidney identifies CC; or (f) administering to a
CC   subject a substrate for RDP, the substrate being labeled with a
CC   detectable moiety, isolating faeces or blood from the subject, and
CC   detecting in the faeces or blood RDP reaction product or RDP substrate
CC   with the detectable moiety, where increased product or decreased
CC   substrate in the faeces or blood indicates CC in the subject. The methods
CC   are useful for detecting colorectal cancer in a subject. The present
CC   sequence is a DNA tag derived from a human transcript whose expression is
CC   elevated in colorectal cancer or colorectal adenoma
XX
SQ   Sequence 10 BP; 2 A; 3 C; 1 G; 4 T; 0 U; 0 Other;
```

```
  Query Match             14.0%;  Score 2.8;  DB 1;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 1.7e+02;
  Matches    4;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CTCCAG 10
              ||  ||
Db          9 CTGGAG 4


RESULT 190
ADL96158
ID   ADL96158 standard; DNA; 10 BP.
XX
AC   ADL96158;
XX
DT   20-MAY-2004  (first entry)
XX
DE   CD15+ myeloid cell associated probe seqid 56.
XX
KW   cytostatic; gene therapy; microarray; gene expression characteristic;
KW   haematopoietic cell; haematopoiesis; myeloid leukaemia; probe;
KW   CD15+ myeloid cell; ss.
XX
OS   Homo sapiens.
XX
PN   US2003165949-A1.
XX
PD   04-SEP-2003.
XX
PF   23-DEC-2002; 2002US-00329465.
XX
PR   27-DEC-2001; 2001US-0343826P.
XX
PA   (WANG/) WANG S M.
PA   (LEES/) LEE S.
PA   (CHEN/) CHEN J.
PA   (ZHOU/) ZHOU G.
PA   (ROWL/) ROWLEY J D.
XX
PI   Wang SM,  Lee S,  Chen J,  Zhou G,  Rowley JD;
XX
DR   WPI; 2003-863699/80.
XX
PT   New microarray for measuring gene expression characteristics of
PT   hematopoietic cells, useful for preparing a composition for diagnosing or
PT   treating myeloid leukemia.
XX
PS   Claim 1; SEQ ID NO 56; 32pp; English.
XX
CC   The invention describes a microarray for measuring gene expression
CC   characteristics of haematopoietic cells comprising at least 5
CC   polynucleotides having distinct sequences. Also described are: a method
CC   of diagnosing or treating an abnormality associated with haematopoiesis;
CC   and diagnosing myeloid leukaemia in a patient. The microarray is useful
CC   for preparing a composition for diagnosing or treating myeloid leukaemia.
CC   This sequence represents a polynucleotide probe comprising a portion of
CC   an expressed gene isolated from a population of CD15+ myeloid cells and
CC   suitable for use in the microarray of the invention.
XX
SQ   Sequence 10 BP; 4 A; 1 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             14.0%;  Score 2.8;  DB 1;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 1.7e+02;
  Matches    4;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CTCCAG 10
              ||  ||
Db          4 CTGGAG 9


RESULT 191
ADI53195/c
ID   ADI53195 standard; DNA; 10 BP.
XX
AC   ADI53195;
XX
DT   22-APR-2004  (first entry)
XX
DE   Human CD3E primer extension primer terminus #29.
XX
KW   Human; CD3 antigen epsilon subunit; CD3E; primer; ss; haplotype;
KW   genotype; primer extension.
XX
OS   Homo sapiens.
XX
PN   US2004018493-A1.
XX
PD   29-JAN-2004.
XX
PF   12-JUL-2002; 2002US-00193507.
XX
PR   12-JUL-2002; 2002US-00193507.
XX
PA   (ANAS/) ANASTASIO A E.
PA   (KAZE/) KAZEMI A.
PA   (LACH/) LACHOWICZ M.
PA   (PABO/) PABON V.
PA   (SHAH/) SHAH N.
XX
PI   Anastasio AE,  Kazemi A,  Lachowicz M,  Pabon V,  Shah N;
XX
DR   WPI; 2004-122016/12.
XX
PT   Haplotyping the CD3 antigen, epsilon subunit (CD3E) gene of an individual
PT   by identifying the phased sequence of nucleotides at polymorphic sites
PT   PS1-PS16 for at least one copy of the individual's CD3E gene.
XX
PS   Claim 22; SEQ ID NO 80; 59pp; English.
XX
CC   The invention relates to haplotyping the CD3 antigen, epsilon subunit
CC   (CD3E) gene of an individual comprising identifying the phased sequence
CC   of nucleotides at polymorphic sites PS1-PS16 for at least one copy of the
CC   individual's CD3E gene and assigning to the individual a CD3E haplotype
CC   or haplotype pair, given in the specification, that is consistent with
CC   the phased sequence. Also included are genotyping the CD3E gene of an
CC   individual, assigning a haplotype pair for the CD3E gene to an
CC   individual, identifying an association between a trait and at least one
CC   haplotype or haplotype pair of the CD3E gene, reducing the potential for
CC   bias in a clinical trial of a candidate drug for treating a disease or
CC   condition predicted to be associated with CD3E activity, an isolated CD3E
CC   polynucleotide, a recombinant nonhuman organism transformed or
CC   transfected with the isolated polynucleotide and expressing a CD3E
CC   protein , an isolated fragment of a CD3E isogene (comprising at least 50
CC   nucleotides in one of the regions of the CD3E gene (ADI53116) and one or
CC   more polymorphisms (P1-P16), where the selected polymorphism has the
CC   position given in the specification), screening for compounds targeting
CC   the CD3E protein to treat a condition or disease predicted to be
CC   associated with CD3E activity, validating the CD3E protein as a candidate
CC   target for treating a medical condition predicted to be associated with
CC   CD3E activity, an isolated oligonucleotide designed to detect a
CC   polymorphism in the CD3E gene at polymorphic sites PS1-PS16, a kit for
CC   haplotyping or genotyping the CD3E gene of an individual and a genome
CC   anthology for the CD3 antigen, epsilon subunit (CD3E) gene which
CC   comprises two or more CD3E isogenes. The method is useful for haplotyping
CC   the CD3 antigen, epsilon subunit (CD3E) gene of an individual for
CC   screening for compounds targeting the CD3E protein to treat a condition
CC   or disease predicted to be associated with CD3E activity. The present
CC   sequence is a Human CD3E primer extension primer terminus.
XX
SQ   Sequence 10 BP; 1 A; 5 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             14.0%;  Score 2.8;  DB 1;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 1.7e+02;
  Matches    4;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
```

```
Qy          5 CTCCAG 10
              ||  ||
Db          9 CTGGAG 4


RESULT 192
ADS77586/c
ID   ADS77586 standard; DNA; 10 BP.
XX
AC   ADS77586;
XX
DT   30-DEC-2004  (first entry)
XX
DE   Breast cancer detection oligonucleotide #1368.
XX
KW   ss; primer; cytostatic; RNA interference; RNAi; gene silencing;
KW   antisense oligonucleotide inhibitor; cathepsin K inhibitor;
KW   cathepsin L inhibitor; cathepsin F inhibitor;
KW   metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
KW   collagen antagonist; diagnosis; breast tissue; cancer.
XX
OS   Homo sapiens.
XX
PN   WO2004085621-A2.
XX
PD   07-OCT-2004.
XX
PF   22-MAR-2004; 2004WO-US008866.
XX
PR   20-MAR-2003; 2003US-0456735P.
XX
PA   (DAND ) DANA FARBER CANCER INST INC.
XX
PI   Polyak K,  Porter D,  Allinen M;
XX
DR   WPI; 2004-728732/71.
XX
PT   Diagnosing breast cancer comprises determining expression levels of a
PT   gene selected from those differentially expressed in normal or cancerous
PT   cells of a breast tissue sample including interleukin 1, thrombospondin 1
PT   and cystatin C.
XX
PS   Example 6; SEQ ID NO 1368; 149pp; English.
XX
CC   The invention relates to a method of diagnosis (M1) comprising: (a)
CC   providing a test sample of breast tissue; (b) determining the level of
CC   expression in the test sample of a gene (e.g. interleukin-8, superoxide
CC   dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
CC   specification, and (c) if the gene is expressed in the test sample at a
CC   lower level than in a control normal breast tissue sample, diagnosing the
CC   test sample as containing cancer cells. The method is used for diagnosing
CC   breast cancer. This sequence corresponds to an oligonucleotide primer
CC   used in the method of the invention.
XX
SQ   Sequence 10 BP; 2 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             14.0%;  Score 2.8;  DB 1;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 1.7e+02;
  Matches    4;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CTCCAG 10
              ||  ||
Db          9 CTGGAG 4


RESULT 193
ADS76686/c
ID   ADS76686 standard; DNA; 10 BP.
XX
AC   ADS76686;
XX
DT   30-DEC-2004  (first entry)
XX
DE   Breast cancer detection oligonucleotide #468.
XX
KW   ss; primer; cytostatic; RNA interference; RNAi; gene silencing;
KW   antisense oligonucleotide inhibitor; cathepsin K inhibitor;
KW   cathepsin L inhibitor; cathepsin F inhibitor;
KW   metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
KW   collagen antagonist; diagnosis; breast tissue; cancer.
XX
OS   Homo sapiens.
XX
PN   WO2004085621-A2.
XX
PD   07-OCT-2004.
XX
PF   22-MAR-2004; 2004WO-US008866.
XX
PR   20-MAR-2003; 2003US-0456735P.
XX
PA   (DAND ) DANA FARBER CANCER INST INC.
XX
PI   Polyak K,  Porter D,  Allinen M;
XX
DR   WPI; 2004-728732/71.
XX
PT   Diagnosing breast cancer comprises determining expression levels of a
PT   gene selected from those differentially expressed in normal or cancerous
PT   cells of a breast tissue sample including interleukin 1, thrombospondin 1
PT   and cystatin C.
XX
PS   Example 2; SEQ ID NO 468; 149pp; English.
XX
CC   The invention relates to a method of diagnosis (M1) comprising: (a)
CC   providing a test sample of breast tissue; (b) determining the level of
CC   expression in the test sample of a gene (e.g. interleukin-8, superoxide
CC   dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
CC   specification, and (c) if the gene is expressed in the test sample at a
CC   lower level than in a control normal breast tissue sample, diagnosing the
CC   test sample as containing cancer cells. The method is used for diagnosing
CC   breast cancer. This sequence corresponds to an oligonucleotide primer
CC   used in the method of the invention.
XX
SQ   Sequence 10 BP; 2 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             14.0%;  Score 2.8;  DB 1;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 1.7e+02;
  Matches    4;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CTCCAG 10
              ||  ||
Db          9 CTGGAG 4


RESULT 194
ADS77754/c
ID   ADS77754 standard; DNA; 10 BP.
XX
AC   ADS77754;
XX
DT   30-DEC-2004  (first entry)
XX
DE   Breast cancer detection oligonucleotide #1536.
XX
KW   ss; primer; cytostatic; RNA interference; RNAi; gene silencing;
KW   antisense oligonucleotide inhibitor; cathepsin K inhibitor;
KW   cathepsin L inhibitor; cathepsin F inhibitor;
KW   metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
KW   collagen antagonist; diagnosis; breast tissue; cancer.
XX
OS   Homo sapiens.
XX
PN   WO2004085621-A2.
XX
PD   07-OCT-2004.
```

```
XX
PF   22-MAR-2004; 2004WO-US008866.
XX
PR   20-MAR-2003; 2003US-0456735P.
XX
PA   (DAND ) DANA FARBER CANCER INST INC.
XX
PI   Polyak K,  Porter D,  Allinen M;
XX
DR   WPI; 2004-728732/71.
XX
PT   Diagnosing breast cancer comprises determining expression levels of a
PT   gene selected from those differentially expressed in normal or cancerous
PT   cells of a breast tissue sample including interleukin 1, thrombospondin 1
PT   and cystatin C.
XX
PS   Example 6; SEQ ID NO 1536; 149pp; English.
XX
CC   The invention relates to a method of diagnosis (M1) comprising: (a)
CC   providing a test sample of breast tissue; (b) determining the level of
CC   expression in the test sample of a gene (e.g. interleukin-8, superoxide
CC   dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
CC   specification, and (c) if the gene is expressed in the test sample at a
CC   lower level than in a control normal breast tissue sample, diagnosing the
CC   test sample as containing cancer cells. The method is used for diagnosing
CC   breast cancer. This sequence corresponds to an oligonucleotide primer
CC   used in the method of the invention.
XX
SQ   Sequence 10 BP; 2 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             14.0%;  Score 2.8;  DB 1;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 1.7e+02;
  Matches    4;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CTCCAG 10
              ||  ||
Db          9 CTGGAG 4


RESULT 195
AAA80951
ID   AAA80951 standard; DNA; 8 BP.
XX
AC   AAA80951;
XX
DT   24-NOV-2000  (first entry)
XX
DE   A. thaliana primer walking octamer SEQ ID NO: 264.
XX
KW   Primer walking; octamer; primer; DNA sequencing; PCR; ss.
XX
OS   Arabidopsis thaliana.
XX
PN   US6083695-A.
XX
PD   04-JUL-2000.
XX
PF   21-MAY-1997;   97US-00859954.
XX
PR   15-APR-1996;   96US-00632782.
XX
PA   (UYHO-) UNIV HOUSTON.
PA   (HARD/) HARDIN S H.
XX
PI   Hardin PE,  Hardin SH,  Homayouni R;
XX
DR   WPI; 2000-474852/41.
XX
PT   Sequencing an unknown DNA molecule for the polymerase chain reaction and
PT   other primer processes comprises primer walking of octamer
PT   oligonucleotides.
XX
PS   Example 8; Col 157-158; 161pp; English.
XX
CC   This invention describes a novel method for sequencing an unknown DNA
CC   molecule which comprises selecting a library primer from an octamer
CC   oligonucleotide library consisting of 48 8-bp sequences and corresponding
CC   complementary sequences, where the library primer is complementary to a
CC   known sequence adjacent to the unknown sequence or is complementary to a
CC   sequence in a known extension product. The method is useful for DNA
CC   nucleotide sequencing, in PCR, and in other processes which make use of
CC   primers. The octamers are used to identify coding sequences. Primer
CC   walking using the octamer libraries is advantageous over other sequencing
CC   methods because it does not require multiple cloning steps nor subsequent
CC   template preparations, and it is a directed and methodical approach.
CC   AAA80688-A81253 represent the octamer primers used in the primer walking
CC   method of the invention
XX
SQ   Sequence 8 BP; 4 A; 1 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             12.0%;  Score 2.4;  DB 1;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 2.8e+02;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTC 12
              || |
Db          5 AGAC 8


RESULT 196
AAA80762
ID   AAA80762 standard; DNA; 8 BP.
XX
AC   AAA80762;
XX
DT   24-NOV-2000  (first entry)
XX
DE   A. thaliana primer walking octamer SEQ ID NO: 75.
XX
KW   Primer walking; octamer; primer; DNA sequencing; PCR; ss.
XX
OS   Arabidopsis thaliana.
XX
PN   US6083695-A.
XX
PD   04-JUL-2000.
XX
PF   21-MAY-1997;   97US-00859954.
XX
PR   15-APR-1996;   96US-00632782.
XX
PA   (UYHO-) UNIV HOUSTON.
PA   (HARD/) HARDIN S H.
XX
PI   Hardin PE,  Hardin SH,  Homayouni R;
XX
DR   WPI; 2000-474852/41.
XX
PT   Sequencing an unknown DNA molecule for the polymerase chain reaction and
PT   other primer processes comprises primer walking of octamer
PT   oligonucleotides.
XX
PS   Example 8; Col 63-64; 161pp; English.
XX
CC   This invention describes a novel method for sequencing an unknown DNA
CC   molecule which comprises selecting a library primer from an octamer
CC   oligonucleotide library consisting of 48 8-bp sequences and corresponding
CC   complementary sequences, where the library primer is complementary to a
CC   known sequence adjacent to the unknown sequence or is complementary to a
CC   sequence in a known extension product. The method is useful for DNA
CC   nucleotide sequencing, in PCR, and in other processes which make use of
CC   primers. The octamers are used to identify coding sequences. Primer
CC   walking using the octamer libraries is advantageous over other sequencing
CC   methods because it does not require multiple cloning steps nor subsequent
CC   template preparations, and it is a directed and methodical approach.
CC   AAA80688-A81253 represent the octamer primers used in the primer walking
```

```
CC   method of the invention
XX
SQ   Sequence 8 BP; 4 A; 1 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             12.0%;  Score 2.4;  DB 1;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 2.8e+02;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTC 12
              || |
Db          3 AGAC 6


RESULT 197
AAS04430
ID   AAS04430 standard; DNA; 10 BP.
XX
AC   AAS04430;
XX
DT   07-SEP-2001  (first entry)
XX
DE   Human DAXX DNA primer-extension oligonucleotide #17.
XX
KW   Death-associated protein 6; DAXX; polymorphism; haplotype pair; human;
KW   immune disorder; autoimmune disease; population diversity; ss;
KW   paternity testing; anthropological lineage; forensic application;
KW   primer-extension oligonucleotide.
XX
OS   Homo sapiens.
XX
PN   WO200125245-A2.
XX
PD   12-APR-2001.
XX
PF   05-OCT-2000; 2000WO-US027487.
XX
PR   06-OCT-1999;   99US-0157909P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Chew A,  Choi JY,  Denton RR,  Nandabalan K,  Stephens JC;
XX
DR   WPI; 2001-308220/32.
XX
PT   New human death-associated protein 6 (DAXX) gene variants comprising 19
PT   polymorphic sites useful in studying the effect of variation on the
PT   biological activity of DAXX and in developing drugs targeting the
PT   protein.
XX
PS   Disclosure; Page 20; 97pp; English.
XX
CC   Sequences AAS04414-AAS04451 represent primer-extension oligonucleotides
CC   specific for a DNA encoding human death-associated protein 6 (DAXX). This
CC   DNA may comprise one or more polymorphisms at specific nucleotide
CC   positions to form one of nineteen possible polymorphic variants.
CC   Associations between a trait and a genotype or a haplotype of the DAXX
CC   gene can be identified by comparing the frequency of the genotype or
CC   haplotype in a population exhibiting the trait with that of a reference
CC   population. A higher frequency in the trait population indicates an
CC   association. Methods involving genotyping or haplotyping of the DAXX gene
CC   of an individual can lead to prediction of haplotype pairs for the DAXX
CC   gene of related individuals, and may be useful in studying the expression
CC   and biological function of DAXX, as well as in developing drugs targeting
CC   this protein. Polymorphic variants of DAXX are useful in studying the
CC   effect of the variation on the biological activity of DAXX as well as on
CC   the binding affinity of candidate drugs targeting DAXX for the treatment
CC   of autoimmune diseases and other immune disorders. Polymorphism is also
CC   useful for studying population diversity, anthropological lineage,
CC   paternity testing, forensic applications, and for identifying
CC   associations between the DAXX genetic variation and a trait such as level
CC   of drug response or susceptibility to disease. DAXX proteins may be used
CC   to measure binding affinities of one or more candidate drugs targeting
CC   the DAXX protein
XX
SQ   Sequence 10 BP; 4 A; 2 C; 4 G; 0 T; 0 U; 0 Other;

  Query Match             12.0%;  Score 2.4;  DB 1;  Length 10;
  Best Local Similarity   75.0%;  Pred. No. 1.8e+02;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTC 12
              || |
Db          5 AGAC 8


RESULT 198
AAF42997/c
ID   AAF42997 standard; DNA; 10 BP.
XX
AC   AAF42997;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11136.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 347; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
```

```
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 0 A; 4 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             12.0%;  Score 2.4;  DB 1;  Length 10;
  Best Local Similarity   75.0%;  Pred. No. 1.8e+02;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 CCAG 10
              | ||
Db          8 CGAG 5


RESULT 199
ADP47134
ID   ADP47134 standard; DNA; 10 BP.
XX
AC   ADP47134;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human phospholipase A2-specific mAb heavy chain DNA sequence #14.
XX
KW   human; monoclonal antibody; phospholipase A2; PLA2;
KW   inflammatory disorder; degenerative disorder;
KW   joint inflammatory reaction; skin inflammatory reaction;
KW   blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
KW   Alzheimer's disease; atherosclerosis; restenosis; heavy chain; ds.
XX
OS   Homo sapiens.
XX
PN   WO2004050850-A2.
XX
PD   17-JUN-2004.
XX
PF   02-DEC-2003; 2003WO-US038234.
XX
PR   02-DEC-2002; 2002US-0430724P.
XX
PA   (ABGE-) ABGENIX INC.
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Landes GM,  Haak-Frendscho M,  Chen L,  Lee YR,  Liang ML,  Feng X;
PI   Jia X,  Nocerini MR;
XX
DR   WPI; 2004-461119/43.
XX
PT   New human monoclonal antibody that binds to phospholipase A2 (PLA2),
PT   useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
PT   asthma, Alzheimer's disease, atherosclerosis, or restenosis.
XX
PS   Example 5; SEQ ID NO 49; 128pp; English.
XX
CC   The invention comprises a human monoclonal antibody that binds to
CC   phospholipase A2 (PLA2). The monoclonal antibody of the invention is
CC   useful in the preparation of a medicament for the treatment of
CC   inflammatory and degenerative disorders stemming from inflammatory
CC   reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
CC   asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
CC   nucleic acid represents a human PLA2-specific monoclonal antibody heavy
CC   chain DNA sequence.
XX
SQ   Sequence 10 BP; 3 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             12.0%;  Score 2.4;  DB 1;  Length 10;
  Best Local Similarity   75.0%;  Pred. No. 1.8e+02;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GTCT 6
              | ||
Db          4 GACT 7


RESULT 200
AAF43826/c
ID   AAF43826 standard; DNA; 10 BP.
XX
AC   AAF43826;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11965.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 377; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 0 A; 3 C; 1 G; 6 T; 0 U; 0 Other;

  Query Match             12.0%;  Score 2.4;  DB 1;  Length 10;
  Best Local Similarity   75.0%;  Pred. No. 1.8e+02;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy          9 AGTC 12
              || |
Db          6 AGAC 3


RESULT 201
AAF41634/c
ID   AAF41634 standard; DNA; 10 BP.
XX
AC   AAF41634;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8373.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 299; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 0 A; 4 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             12.0%;  Score 2.4;  DB 1;  Length 10;
  Best Local Similarity   75.0%;  Pred. No. 1.8e+02;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTC 12
              || |
Db          8 AGAC 5


RESULT 202
AAS95397
ID   AAS95397 standard; DNA; 10 BP.
XX
AC   AAS95397;
XX
DT   14-FEB-2002  (first entry)
XX
DE   Human ICAM2 gene allele-specific oligonucleotide PCR primer #2.
XX
KW   Human; intercellular adhesion molecule 2; ICAM2; haplotyping; ss;
KW   haplotype pair; single nucleotide polymorphism; genotyping; PCR primer;
KW   gene therapy; drug screening; anti-HIV; antiinflammatory; probe;
KW   human immunodeficiency virus; sequencing primer.
XX
OS   Homo sapiens.
XX
PN   WO200185918-A1.
XX
PD   15-NOV-2001.
XX
PF   07-MAY-2001; 2001WO-US014714.
XX
PR   05-MAY-2000; 2000US-0201946P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Chew A,  Choi JY,  Denton RR,  Kliem SE,  Lee HH,  Nandabalan K;
XX
DR   WPI; 2002-055590/07.
XX
PT   Novel polynucleotide containing polymorphisms in intercellular adhesion
PT   molecule 2 gene, useful in developing drugs for treating human
PT   immunodeficiency virus infection and inflammatory diseases.
XX
PS   Claim 18; Page 13; 81pp; English.
XX
CC   The invention relates to single nucleotide polymorphisms in the gene
CC   encoding human intercellular adhesion molecule 2 (ICAM2). A method for
CC   haplotyping the ICAM2 gene in an individual comprises identifying the
CC   nucleotide at one or more polymorphic sites and determining whether one
CC   of the copies of the gene is defined by one of the ICAM2 haplotypes given
CC   in the specification or whether both copies are defined by a haplotype
CC   pair. This method is useful in genotyping, whereby all possible haplotype
CC   pairs can be assigned to specific genotypes. An association between a
CC   trait and a haplotype or haplotype pair of the ICAM2 gene can be
CC   identified by comparing the frequency of the haplotype or haplotype pair
CC   in a population exhibiting the trait with the frequency of the haplotype
CC   or haplotype pair in a reference population, where a higher haplotype
CC   frequency in the trait population indicates the trait is associated with
CC   the haplotype or haplotype pair. ICAM2 and its corresponding DNA are used
CC   for studying the expression and function of ICAM2, for use in screening
CC   for candidate drugs to treat diseases related to ICAM2 activity, such as
CC   HIV infection and inflammatory diseases. The sequences are also useful
CC   for studying the effect of variation on the biological activity of ICAM2
CC   as well as on the binding affinity of candidate drugs targeting ICAM2.
CC   Sequences AAS95362-AAS95417 and AAS95419-AAS95442 represent allele-
CC   specific oligonucleotide probes, sequencing primers, PCR primers and cDNA
CC   encoding human ICAM2
XX
SQ   Sequence 10 BP; 4 A; 1 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             12.0%;  Score 2.4;  DB 1;  Length 10;
  Best Local Similarity   75.0%;  Pred. No. 1.8e+02;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy          9 AGTC 12
              || |
Db          5 AGAC 8
```

```
RESULT 203
AAS97350/c
ID   AAS97350 standard; DNA; 10 BP.
XX
AC   AAS97350;
XX
DT   12-MAR-2002  (first entry)
XX
DE   Human CRYBB1 gene ASO primer extension PCR primer 3' end #9.
XX
KW   Human; crystallin beta B1; CRYBB1; chromosome 22q12.1; ophthalmalogical;
KW   cataract; allele specific oligonucleotide; ASO; ss; haplotype;
KW   genotyping; transgenic animal; PCR primer; primer extension.
XX
OS   Homo sapiens.
XX
PN   WO200185998-A1.
XX
PD   15-NOV-2001.
XX
PF   07-MAY-2001; 2001WO-US014715.
XX
PR   05-MAY-2000; 2000US-0202253P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Choi JY,  Kazemi A,  Kliem SE,  Koshy B,  Rounds E;
XX
DR   WPI; 2002-062253/08.
XX
PT   Novel polymorphic variants of crystallin, beta B1 useful in studying
PT   expression and function of the protein, useful for screening candidate
PT   drugs to treat diseases e.g. cataract.
XX
PS   Claim 17; Page 13; 94pp; English.
XX
CC   The invention relates to an isolated polynucleotide comprising a sequence
CC   which is a polymorphic variant of a reference sequence for crystallin,
CC   beta B1 (CRYBB1, located on chromosome 22q12.1) gene or their fragment,
CC   where the polymorphic variant comprises a CRYBB1 isogene defined by a
CC   haplotype from haplotypes 1-16 as given in the specification. Also
CC   included are a transgenic non-human animal transformed or transfected
CC   with the polymorphic variant, a computer system for storing and analysing
CC   polymorphism data for CRYBB1 gene, a genome anthology for the CRYBB1 gene
CC   which comprises the defined CRYBB1 isogenes, methods of determining an
CC   individuals haplotype or genotype as well as methods of determining the
CC   association of a particular haplotype with a disease or trait and a
CC   composition comprising at least one genotyping oligonucleotide
CC   (especially allele-specific oligonucleotides (ASO)) for detecting a
CC   polymorphism in the CRYBB1. The isogenes or haplotypes are useful for
CC   improving the efficiency and reliability of several steps in the
CC   discovery and development of drugs for treating diseases associated with
CC   CRYBB1 activity, e.g. cataract. and can also be used by the
CC   pharmaceutical research scientist to validate CRYBB1 as a candidate
CC   target for, and in design of clinical trials of candidate drugs for,
CC   treating a specific condition drugs or disease predicted to be associated
CC   with CRYBB1 activity. The ASOs are useful as probes and primers, and for
CC   assaying a polymorphism in the target region. The present sequence is the
CC   allele specific 3' end of a PCR primer used in primer extension
CC   experiment to detect polymorphisms in CRYBB1
XX
SQ   Sequence 10 BP; 0 A; 4 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match           12.0%;  Score 2.4;  DB 1;  Length 10;
  Best Local Similarity  75.0%;  Pred. No. 1.8e+02;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy          9 AGTC 12
              || |
Db          6 AGAC 3
```

```
RESULT 204
ABF03676
ID   ABF03676 standard; DNA; 13 BP.
XX
AC   ABF03676;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 103673 for detecting SNP TSC0025934.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 103673; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 5 A; 1 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match           12.0%;  Score 2.4;  DB 1;  Length 13;
  Best Local Similarity  75.0%;  Pred. No. 1.6e+02;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy          9 AGTC 12
              || |
Db          4 AGAC 7
```

```
RESULT 205
ABF03677/c
ID   ABF03677 standard; DNA; 13 BP.
XX
AC   ABF03677;
XX
DT   21-FEB-2002  (first entry)
XX
```

```
DE   Oligonucleotide SEQ ID NO 103674 for detecting SNP TSC0025934.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 103674; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 1 A; 6 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             12.0%;  Score 2.4;  DB 1;  Length 13;
  Best Local Similarity   75.0%;  Pred. No. 1.6e+02;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTC 12
              || |
Db         10 AGAC 7


RESULT 206
ADQ33489
ID   ADQ33489 standard; DNA; 11 BP.
XX
AC   ADQ33489;
XX
DT   23-SEP-2004  (first entry)
XX
DE   Human facial skin-associated DNA fragment SEQ ID NO 1579.
XX
KW   facial skin; human; serial analysis of gene expression; SAGE;
KW   homeostasis; biochip; cosmetic; pharmaceutical; ds.
XX
OS   Homo sapiens.
XX
PN   DE10260928-A1.
XX
PD   08-JUL-2004.
XX
PF   20-DEC-2002; 2002DE-01060928.
XX
PR   20-DEC-2002; 2002DE-01060928.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Schlotmann K,  Gassenmeier T,  Holtkoetter O;
PI   Conradt M,  Hofmann K;
XX
DR   WPI; 2004-518855/50.
XX
PT   In vitro identification of genes important for facial skin, useful for
PT   assessing homeostasis and in screening for pharmaceutical or cosmetic
PT   agents, based on differential expression analysis.
XX
PS   Claim 5; SEQ ID NO 1579; 577pp; German.
XX
CC   This invention describes a novel in vitro method for identifying genes
CC   that are significant for facial skin in humans. The method comprises
CC   recovering, from facial skin, a first mixture of genetically expressed
CC   (transcribed and optionally translated) factors (i.e. proteins, mRNA or
CC   their fragments), recovering a second, similar mixture from some other
CC   human tissue, preferably skin from a protected area, especially from the
CC   breast and subjecting the mixtures to serial analysis of gene expression
CC   (SAGE) to identify those genes for which expression is markedly different
CC   between facial skin and the other tissue. The invention also describes an
CC   in vitro method for determining homeostasis of human facial skin; a test
CC   kit which comprises a solid support (flexible or rigid) on which are
CC   immobilised probes that bind specifically to the factors of interest and
CC   a biochip for determining homeostasis of human facial skin. The products
CC   of the invention are also used in a method which determines activity of
CC   cosmetic and pharmaceutical agents for use against disorders or
CC   disturbances of the homeostasis of human skin and a screening method for
CC   identifying cosmetic and pharmaceutical agents. The method allows
CC   identification of as many as possible of the genes important for facial
CC   skin and thus of a very wide range of potential therapeutic and cosmetic
CC   agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to
CC   identify the facial skin-associated genes described in the invention.
XX
SQ   Sequence 11 BP; 5 A; 1 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             11.0%;  Score 2.2;  DB 1;  Length 11;
  Best Local Similarity   57.1%;  Pred. No. 1.8e+02;
  Matches    4;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          9 AGTCTCT 15
              ||   ||
Db          3 AGAAACT 9


RESULT 207
AAF38748
ID   AAF38748 standard; DNA; 10 BP.
XX
AC   AAF38748;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5487.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
```

```
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 196; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 5 A; 1 C; 4 G; 0 T; 0 U; 0 Other;

  Query Match             10.0%;  Score 2;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 CG 18
              ||
Db          3 CG 4


RESULT 208
AAF38731
ID   AAF38731 standard; DNA; 10 BP.
XX
AC   AAF38731;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5470.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;  99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 195; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 7 A; 1 C; 2 G; 0 T; 0 U; 0 Other;

  Query Match             10.0%;  Score 2;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 CG 18
              ||
Db          3 CG 4


RESULT 209
AAF33728
ID   AAF33728 standard; DNA; 10 BP.
XX
AC   AAF33728;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:467.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
```

PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Claim 1; Page 391; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 5 A; 0 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 10.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AG 10
||
Db 3 AG 4

RESULT 210
AAF34632
ID AAF34632 standard; DNA; 10 BP.
XX
AC AAF34632;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1371.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.

XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 49; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 5 A; 0 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 10.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AG 10
||
Db 3 AG 4

RESULT 211
AAF36782/c
ID AAF36782 standard; DNA; 10 BP.
XX
AC AAF36782;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3521.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;

KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 125; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 1 A; 2 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 10.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 CG 18
||
Db 6 CG 5

RESULT 212
ADG64354
ID ADG64354 standard; DNA; 11 BP.
XX
AC ADG64354;
XX
DT 11-MAR-2004 (first entry)
XX
DE DNA polymerase 3'-5' exonuclease domain related PCR primer SEQ ID NO:39.
XX
KW thermostable DNA polymerase; thermoactive DNA polymerase;
KW 3'-5' exonuclease domain; mutagenesis; genetic engineering;
KW genetic fingerprinting; forensic; cloning; infectious agent;
KW genetic disease; DNA polymerase; PCR primer; ss.
XX
OS Synthetic.
XX
PN EP1350841-A2.
XX
PD 08-OCT-2003.
XX
PF 31-MAR-2003; 2003EP-00006888.
XX
PR 02-APR-2002; 2002US-0369815P.
XX
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Schoenbrunner NJ, Myers TW, Gelfland DH;
XX
DR WPI; 2003-815070/77.
XX
PT New thermostable or thermoactive DNA polymerases with attenuated 3'-5'
PT exonuclease activity, useful in polymerase chain reaction for in vitro
PT mutagenesis and engineering of DNA, or genetic fingerprinting of forensic
PT samples.
XX
PS Example 1; SEQ ID NO 39; 80pp; English.
XX
CC The present invention describes an isolated thermostable or thermoactive
CC DNA polymerase. The DNA polymerase comprises: (a) a 3'-5' exonuclease
CC domain which exhibits an attenuated 3'-5' exonuclease activity of about
CC 6.5 or less, but greater than 0, u/pmol, measured using the Standard
CC Assay; or (b) a 3'-5' exonuclease domain, and having a 5'-3' polymerase
CC activity and an attenuated 3'-5' exonuclease activity, where the ratio of
CC the 5'-3' polymerase activity in u/pmol to the 3'-5' exonuclease activity
CC in u/pmol is about 100-1. The thermostable or thermoactive DNA
CC polymerases are useful in recombinant DNA techniques or polymerase chain
CC reaction for in vitro mutagenesis and engineering of DNA, genetic
CC fingerprinting of forensic samples, direct cloning from genomic DNA or
CC cDNA, assays for the presence of infectious agents, or parental diagnosis
CC of genetic disease. The DNA polymerase provides a significant improvement
CC over thermostable or thermoactive DNA polymerases of prior art. The
CC present DNA polymerases reduce degradation of primers as compared to wild
CC type thermostable or thermoactive DNA polymerases. The DNA polymerases
CC can be easily and efficiently expressed to a high level in a recombinant
CC expression system, which facilitates commercial production of the enzyme,
CC and they readily incorporate nucleoside triphosphate analogues, in
CC contrast to thermostable archae proofreading DNA polymerase. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 11 BP; 5 A; 2 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 10.0%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 CG 18
||
Db 1 CG 2

Search completed: April 23, 2006, 11:43:24
Job time : 1 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 23, 2006, 11:44:44 ; Search time 0.001 Seconds
(without alignments)
9.040 Million cell updates/sec

Title: US-10-728-399-1
Perfect score: 20
Sequence: 1 ttgtctccagtctcttcgtt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 24 seqs, 226 residues

Total number of hits satisfying chosen parameters: 48

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : rni.subdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	13.8	69.0	17	1	US-09-866-108A-9344	Sequence 9344, Ap
c	2	13.8	69.0	17	1	US-09-866-108A-9345	Sequence 9345, Ap
c	3	13.8	69.0	17	1	US-09-866-108A-9346	Sequence 9346, Ap
	4	8.4	42.0	10	1	US-08-701-270-9	Sequence 9, Appli
c	5	8.4	42.0	10	1	US-09-579-536C-43	Sequence 43, Appl
c	6	8	40.0	8	1	US-08-859-954-75	Sequence 75, Appl
c	7	8	40.0	8	1	US-08-859-954-264	Sequence 264, App
c	8	8	40.0	8	1	US-08-859-954-501	Sequence 501, App
c	9	8	40.0	10	1	US-10-042-111-9	Sequence 9, Appli
	10	7.4	37.0	9	1	US-08-605-163-16	Sequence 16, Appl
	11	7	35.0	8	1	US-08-859-954-44	Sequence 44, Appl
c	12	7	35.0	8	1	US-08-859-954-74	Sequence 74, Appl
	13	7	35.0	8	1	US-08-859-954-177	Sequence 177, App
c	14	7	35.0	8	1	US-08-859-954-198	Sequence 198, App
c	15	7	35.0	8	1	US-08-859-954-199	Sequence 199, App
c	16	7	35.0	8	1	US-08-859-954-263	Sequence 263, App
c	17	7	35.0	8	1	US-08-859-954-357	Sequence 357, App
	18	7	35.0	8	1	US-08-859-954-370	Sequence 370, App
c	19	7	35.0	8	1	US-08-859-954-401	Sequence 401, App
c	20	7	35.0	8	1	US-08-859-954-491	Sequence 491, App
c	21	7	35.0	8	1	US-08-859-954-500	Sequence 500, App
c	22	7	35.0	8	1	US-08-859-954-566	Sequence 566, App
	23	7	35.0	8	1	US-09-910-469-43	Sequence 43, Appl
c	24	7	35.0	8	1	US-09-910-469-44	Sequence 44, Appl
c	25	4.8	24.0	9	1	US-08-605-163-16	Sequence 16, Appl
c	26	4.4	22.0	8	1	US-08-859-954-177	Sequence 177, App
	27	4.2	21.0	10	1	US-10-042-111-9	Sequence 9, Appli
	28	3.8	19.0	8	1	US-08-859-954-198	Sequence 198, App
	29	3.8	19.0	8	1	US-08-859-954-500	Sequence 500, App
	30	3.4	17.0	8	1	US-08-859-954-199	Sequence 199, App
	31	3.4	17.0	8	1	US-08-859-954-357	Sequence 357, App
c	32	3.4	17.0	8	1	US-08-859-954-370	Sequence 370, App
	33	3.4	17.0	8	1	US-08-859-954-491	Sequence 491, App
c	34	3.4	17.0	8	1	US-09-910-469-43	Sequence 43, Appl
	35	3.4	17.0	8	1	US-09-910-469-44	Sequence 44, Appl
	36	3.4	17.0	17	1	US-09-866-108A-9344	Sequence 9344, Ap
	37	3.4	17.0	17	1	US-09-866-108A-9345	Sequence 9345, Ap
	38	3.4	17.0	17	1	US-09-866-108A-9346	Sequence 9346, Ap
	39	3	15.0	8	1	US-08-859-954-566	Sequence 566, App
c	40	3	15.0	10	1	US-08-701-270-9	Sequence 9, Appli
	41	2.8	14.0	8	1	US-08-859-954-501	Sequence 501, App
	42	2.4	12.0	8	1	US-08-859-954-75	Sequence 75, Appl
	43	2.4	12.0	8	1	US-08-859-954-264	Sequence 264, App
c	44	2.4	12.0	8	1	US-08-859-954-44	Sequence 44, Appl
	45	2.4	12.0	8	1	US-08-859-954-74	Sequence 74, Appl
	46	2.4	12.0	8	1	US-08-859-954-401	Sequence 401, App
	47	2	10.0	8	1	US-08-859-954-263	Sequence 263, App
	48	2	10.0	10	1	US-09-579-536C-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-09-866-108A-9344/c
; Sequence 9344, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9344
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9344

Query Match 69.0%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 0.6;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          4 TCTCCAGTCTCTTCGTT 20
              || |||| |||||||||
Db         17 TCCCCAGCCTCTTCGTT 1
```

```
RESULT 2
US-09-866-108A-9345/c
; Sequence 9345, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108A
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 15755
;  SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9345
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108A-9345

  Query Match             69.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 0.6;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAGTCTCTTCGT 19
              ||| |||| ||||||||
Db         17 GTCCCCAGCCTCTTCGT 1


RESULT 3
US-09-866-108A-9346/c
; Sequence 9346, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108A
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 15755
;  SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9346
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108A-9346

  Query Match             69.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 0.6;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TGTCTCCAGTCTCTTCG 18
              |||| |||| |||||||
Db         17 TGTCCCCAGCCTCTTCG 1


RESULT 4
US-08-701-270-9
; Sequence 9, Application US/08701270
; Patent No. 5702926
;  GENERAL INFORMATION:
;    APPLICANT:  Fraiser, Melinda S.
;    APPLICANT:  Walker, George T.
;    TITLE OF INVENTION:  STRAND DISPLACEMENT AMPLIFICATION USING
;    TITLE OF INVENTION:  BORONATED NUCLEOTIDES
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Richard J. Rodrick, Becton Dickinson and
;      ADDRESSEE:  Company
;      STREET:  1 Becton Drive
;      CITY:  Franklin Lakes
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07417
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/701,270
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fugit, Donna R.
;      REGISTRATION NUMBER:  32,135
;      REFERENCE/DOCKET NUMBER:  P-3556
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
```

```
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-701-270-9

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 4.3;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAGTC 12
              ||||||| ||
Db          1 GTCTCCAATC 10


RESULT 5
US-09-579-536C-43/c
; Sequence 43, Application US/09579536C
; Patent No. 6716974
; GENERAL INFORMATION:
;  APPLICANT: MACIAG, Thomas
;  APPLICANT:  ZIMRIN, Ann
;  APPLICANT:  SMALL, Deena
;  APPLICANT:  PRUDOVSKY, Igor
;  TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC METHODS AND COMPOSITIONS BASED ON JAGG
;  TITLE OF INVENTION:  PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: 053689-5002-01
;  CURRENT APPLICATION NUMBER: US/09/579,536C
;  CURRENT FILING DATE:  2000-05-24
;  PRIOR APPLICATION NUMBER: US 09/199,865
;  PRIOR FILING DATE: 1998-11-25
;  PRIOR APPLICATION NUMBER: PCT/US97/09407
;  PRIOR FILING DATE: 1997-05-30
;  PRIOR APPLICATION NUMBER: US 60/018,841
;  PRIOR FILING DATE: 1996-05-31
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-579-536C-43

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 4.3;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 TCTCTTCGTT 20
              ||||||| ||
Db         10 TCTCTTCCTT 1


RESULT 6
US-08-859-954-75/c
; Sequence 75, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  75:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-75

  Query Match             40.0%;  Score 8;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTGTCTCC 8
              ||||||||
Db          8 TTGTCTCC 1


RESULT 7
US-08-859-954-264/c
; Sequence 264, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
```

```
;  INFORMATION FOR SEQ ID NO:  264:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-264

  Query Match             40.0%;  Score 8;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GTCTCTTC 17
               ||||||||
Db          8 GTCTCTTC 1


RESULT 8
US-08-859-954-501/c
; Sequence 501, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  501:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-501

  Query Match             40.0%;  Score 8;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TCTCCAGT 11
              ||||||||
Db          8 TCTCCAGT 1


RESULT 9
US-10-042-111-9/c
; Sequence 9, Application US/10042111
; Patent No. 6551476
; GENERAL INFORMATION:
;  APPLICANT: ZHEJIANG ACADEMY OF AGRICULTURAL SCIENCES
;  APPLICANT:  CHEN, Jinqing
;  TITLE OF INVENTION: A METHOD FOR CONTROLLING RATIO OF PROTEINS/LIPIDS IN CROP SEEDS
;  FILE REFERENCE: ref.
;  CURRENT APPLICATION NUMBER: US/10/042,111
;  CURRENT FILING DATE:  2002-05-08
;  PRIOR APPLICATION NUMBER: CN 99124511.3
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: primer
US-10-042-111-9

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 4.7;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CTCCAGTC 12
              ||||||||
Db          9 CTCCAGTC 2


RESULT 10
US-08-605-163-16
; Sequence 16, Application US/08605163
; Patent No. 5879886
;  GENERAL INFORMATION:
;    APPLICANT:  Meo, Tommaso
;    APPLICANT:  Tosi, Mario
;    APPLICANT:  Verpy, Elisabeth
;    APPLICANT:  Biasotto, Michel
;    TITLE OF INVENTION:  Method for Detecting Molecules
;    TITLE OF INVENTION:  Containing Nucleotide Mismatches and the Location of These
;    TITLE OF INVENTION:  Mismatches, and Application to the Detection of Base
;    TITLE OF INVENTION:  Substitutions or Deletions in Nucleotide Sequences.
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/605,163
;      FILING DATE:  08-MAR-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Kenneth J.
;      REGISTRATION NUMBER:  25,146
```

```
;      REFERENCE/DOCKET NUMBER:  05986.0005-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 408-4000
;      TELEFAX:  (202) 408-4400
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-605-163-16

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 18;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TGTCTCCAG 10
              || ||||||
Db          1 TGACTCCAG 9


RESULT 11
US-08-859-954-44
; Sequence 44, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  44:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-44

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GTCTCTT 16
              |||||||
Db          2 GTCTCTT 8


RESULT 12
US-08-859-954-74/c
; Sequence 74, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  74:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-74

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TGTCTCC 8
              |||||||
Db          7 TGTCTCC 1


RESULT 13
US-08-859-954-177
; Sequence 177, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
```

```
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  177:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-177

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 AGTCTCT 15
              |||||||
Db          2 AGTCTCT 8


RESULT 14
US-08-859-954-198/c
; Sequence 198, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  198:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-198

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CAGTCTC 14
              |||||||
Db          7 CAGTCTC 1


RESULT 15
US-08-859-954-199/c
; Sequence 199, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  199:
```

```
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-199

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CAGTCTC 14
              |||||||
Db          7 CAGTCTC 1


RESULT 16
US-08-859-954-263/c
; Sequence 263, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  263:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-263

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 TCTCTTC 17
              |||||||
Db          7 TCTCTTC 1


RESULT 17
US-08-859-954-357/c
; Sequence 357, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  357:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-357

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GTCTCCA 9
              |||||||
Db          7 GTCTCCA 1


RESULT 18
US-08-859-954-370
; Sequence 370, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
```

```
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  370:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-370

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CCAGTCT 13
              |||||||
Db          1 CCAGTCT 7


RESULT 19
US-08-859-954-401/c
; Sequence 401, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  401:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-401

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GTCTCCA 9
              |||||||
Db          8 GTCTCCA 2


RESULT 20
US-08-859-954-491/c
; Sequence 491, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  491:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
```

```
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-491

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CCAGTCT 13
              |||||||
Db          7 CCAGTCT 1


RESULT 21
US-08-859-954-500/c
; Sequence 500, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  500:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-500

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CTCCAGT 11
              |||||||
Db          7 CTCCAGT 1


RESULT 22
US-08-859-954-566/c
; Sequence 566, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  566:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-566

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GTCTCCA 9
              |||||||
Db          8 GTCTCCA 2


RESULT 23
US-09-910-469-43
; Sequence 43, Application US/09910469
; Patent No. 6893822
; GENERAL INFORMATION:
;  APPLICANT: Schweitzer, Markus
;  APPLICANT:  Anderson, Richard R.
;  APPLICANT:  Mueller, Jochen
;  APPLICANT:  Fiechtner, Michael
;  APPLICANT:  Bruecher, Christoph
;  APPLICANT:  Kienle, Stefan
;  APPLICANT:  Orwick, Jill
```

```
;  APPLICANT:  Pignot, Marc
;  APPLICANT:  Raddatz, Stefan
;  APPLICANT:  Schneider, Eberhard
;  APPLICANT:  Windhab, No. 6893822bert
;  TITLE OF INVENTION: Sorting and Immobilization System for Nucleic Acids Using Synthet
;  TITLE OF INVENTION:  Binding Systems
;  FILE REFERENCE: 264/217 Nanogen Recognomics
;  CURRENT APPLICATION NUMBER: US/09/910,469
;  CURRENT FILING DATE:  2001-07-19
;  NUMBER OF SEQ ID NOS: 184
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
;   LENGTH: 8
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic binding system
;   NAME/KEY: modified_base
;   LOCATION: (1)..(8)
;   OTHER INFORMATION: pyranosyl RNA
US-09-910-469-43

  Query Match            35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 20;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CCAGTCT 13
              |||||||
Db          1 CCAGTCT 7


RESULT 24
US-09-910-469-44/c
; Sequence 44, Application US/09910469
; Patent No. 6893822
; GENERAL INFORMATION:
;  APPLICANT: Schweitzer, Markus
;  APPLICANT:  Anderson, Richard R.
;  APPLICANT:  Mueller, Jochen
;  APPLICANT:  Fiechtner, Michael
;  APPLICANT:  Bruecher, Christoph
;  APPLICANT:  Kienle, Stefan
;  APPLICANT:  Orwick, Jill
;  APPLICANT:  Pignot, Marc
;  APPLICANT:  Raddatz, Stefan
;  APPLICANT:  Schneider, Eberhard
;  APPLICANT:  Windhab, No. 6893822bert
;  TITLE OF INVENTION: Sorting and Immobilization System for Nucleic Acids Using Synthet
;  TITLE OF INVENTION:  Binding Systems
;  FILE REFERENCE: 264/217 Nanogen Recognomics
;  CURRENT APPLICATION NUMBER: US/09/910,469
;  CURRENT FILING DATE:  2001-07-19
;  NUMBER OF SEQ ID NOS: 184
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
;   LENGTH: 8
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic binding system
;   NAME/KEY: modified_base
;   LOCATION: (1)..(8)
;   OTHER INFORMATION: pyranosyl RNA
US-09-910-469-44

  Query Match            35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 20;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CCAGTCT 13
              |||||||
Db          8 CCAGTCT 2


RESULT 25
US-08-605-163-16/c
; Sequence 16, Application US/08605163
; Patent No. 5879886
;  GENERAL INFORMATION:
;    APPLICANT:  Meo, Tommaso
;    APPLICANT:  Tosi, Mario
;    APPLICANT:  Verpy, Elisabeth
;    APPLICANT:  Biasotto, Michel
;    TITLE OF INVENTION:  Method for Detecting Molecules
;    TITLE OF INVENTION:  Containing Nucleotide Mismatches and the Location of These
;    TITLE OF INVENTION:  Mismatches, and Application to the Detection of Base
;    TITLE OF INVENTION:  Substitutions or Deletions in Nucleotide Sequences.
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/605,163
;      FILING DATE:  08-MAR-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Kenneth J.
;      REGISTRATION NUMBER:  25,146
;      REFERENCE/DOCKET NUMBER:  05986.0005-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 408-4000
;      TELEFAX:  (202) 408-4400
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-605-163-16

  Query Match            24.0%;  Score 4.8;  DB 1;  Length 9;
  Best Local Similarity  75.0%;  Pred. No. 18;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CTCCAGTC 12
              ||  ||||
Db          9 CTGGAGTC 2


RESULT 26
US-08-859-954-177/c
; Sequence 177, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
```

```
;       COUNTRY:  U.S.A.
;       ZIP:  77010-3095
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/859,954
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/632,782
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Paul, Thomas D.
;       REGISTRATION NUMBER:  32,714
;       REFERENCE/DOCKET NUMBER:  D-5900
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  713/651-5325
;       TELEFAX:  713/651-5246
;   INFORMATION FOR SEQ ID NO:  177:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  8 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  other nucleic acid
;       DESCRIPTION:  /desc = "oligonucleotide"
;     HYPOTHETICAL:  YES
;     ANTI-SENSE:  YES
US-08-859-954-177

  Query Match             22.0%;  Score 4.4;  DB 1;  Length 8;
  Best Local Similarity   83.3%;  Pred. No. 20;
  Matches    5;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCTC 14
              || |||
Db          6 AGACTC 1


RESULT 27
US-10-042-111-9
; Sequence 9, Application US/10042111
; Patent No. 6551476
; GENERAL INFORMATION:
;  APPLICANT: ZHEJIANG ACADEMY OF AGRICULTURAL SCIENCES
;  APPLICANT:  CHEN, Jinqing
;  TITLE OF INVENTION: A METHOD FOR CONTROLLING RATIO OF PROTEINS/LIPIDS IN CROP SEEDS
;  FILE REFERENCE: ref.
;  CURRENT APPLICATION NUMBER: US/10/042,111
;  CURRENT FILING DATE:  2002-05-08
;  PRIOR APPLICATION NUMBER: CN 99124511.3
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: primer
US-10-042-111-9

  Query Match             21.0%;  Score 4.2;  DB 1;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 10;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAGT 11
              | ||  |||
Db          2 GACTGGAGT 10


RESULT 28
US-08-859-954-198
; Sequence 198, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
;     APPLICANT:  Hardin, Susan H.
;     APPLICANT:  Homayouni, Ramin
;     APPLICANT:  Hardin, Paul E.
;     TITLE OF INVENTION:  Design and Optimized Primer Library for
;     TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;     NUMBER OF SEQUENCES:  566
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Fulbright & Jaworski L.L.P.
;       STREET:  1301 McKinney, Suite 5100
;       CITY:  Houston
;       STATE:  Texas
;       COUNTRY:  U.S.A.
;       ZIP:  77010-3095
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/859,954
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/632,782
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Paul, Thomas D.
;       REGISTRATION NUMBER:  32,714
;       REFERENCE/DOCKET NUMBER:  D-5900
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  713/651-5325
;       TELEFAX:  713/651-5246
;   INFORMATION FOR SEQ ID NO:  198:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  8 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  other nucleic acid
;       DESCRIPTION:  /desc = "oligonucleotide"
;     HYPOTHETICAL:  YES
;     ANTI-SENSE:  YES
US-08-859-954-198

  Query Match             19.0%;  Score 3.8;  DB 1;  Length 8;
  Best Local Similarity   71.4%;  Pred. No. 20;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          9 AGTCTCT 15
              || || |
Db          2 AGACTGT 8


RESULT 29
US-08-859-954-500
; Sequence 500, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
;     APPLICANT:  Hardin, Susan H.
;     APPLICANT:  Homayouni, Ramin
;     APPLICANT:  Hardin, Paul E.
;     TITLE OF INVENTION:  Design and Optimized Primer Library for
;     TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;     NUMBER OF SEQUENCES:  566
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Fulbright & Jaworski L.L.P.
```

```
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  500:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-500

  Query Match             19.0%;  Score 3.8;  DB 1;  Length 8;
  Best Local Similarity   71.4%;  Pred. No. 20;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CTCCAGT 11
              ||  |||
Db          2 CTGGAGT 8


RESULT 30
US-08-859-954-199
; Sequence 199, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  199:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-199

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 8;
  Best Local Similarity   80.0%;  Pred. No. 20;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          2 AGACT 6


RESULT 31
US-08-859-954-357
; Sequence 357, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  357:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
```

```
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-357

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 8;
  Best Local Similarity   80.0%;  Pred. No. 20;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          4 AGACT 8


RESULT 32
US-08-859-954-370/c
; Sequence 370, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  370:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-370

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 8;
  Best Local Similarity   80.0%;  Pred. No. 20;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          7 AGACT 3


RESULT 33
US-08-859-954-491
; Sequence 491, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  491:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-491

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 8;
  Best Local Similarity   80.0%;  Pred. No. 20;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          1 AGACT 5


RESULT 34
US-09-910-469-43/c
; Sequence 43, Application US/09910469
; Patent No. 6893822
; GENERAL INFORMATION:
;  APPLICANT: Schweitzer, Markus
;  APPLICANT:  Anderson, Richard R.
;  APPLICANT:  Mueller, Jochen
;  APPLICANT:  Fiechtner, Michael
;  APPLICANT:  Bruecher, Christoph
;  APPLICANT:  Kienle, Stefan
;  APPLICANT:  Orwick, Jill
;  APPLICANT:  Pignot, Marc
;  APPLICANT:  Raddatz, Stefan
;  APPLICANT:  Schneider, Eberhard
```

```
;  APPLICANT:  Windhab, No. 6893822bert
;  TITLE OF INVENTION: Sorting and Immobilization System for Nucleic Acids Using Synthet
;  TITLE OF INVENTION:  Binding Systems
;  FILE REFERENCE: 264/217 Nanogen Recognomics
;  CURRENT APPLICATION NUMBER: US/09/910,469
;  CURRENT FILING DATE:  2001-07-19
;  NUMBER OF SEQ ID NOS: 184
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
;   LENGTH: 8
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic binding system
;   NAME/KEY: modified_base
;   LOCATION: (1)..(8)
;   OTHER INFORMATION: pyranosyl RNA
US-09-910-469-43

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 8;
  Best Local Similarity   80.0%;  Pred. No. 20;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          7 AGACT 3


RESULT 35
US-09-910-469-44
; Sequence 44, Application US/09910469
; Patent No. 6893822
; GENERAL INFORMATION:
;  APPLICANT: Schweitzer, Markus
;  APPLICANT:  Anderson, Richard R.
;  APPLICANT:  Mueller, Jochen
;  APPLICANT:  Fiechtner, Michael
;  APPLICANT:  Bruecher, Christoph
;  APPLICANT:  Kienle, Stefan
;  APPLICANT:  Orwick, Jill
;  APPLICANT:  Pignot, Marc
;  APPLICANT:  Raddatz, Stefan
;  APPLICANT:  Schneider, Eberhard
;  APPLICANT:  Windhab, No. 6893822bert
;  TITLE OF INVENTION: Sorting and Immobilization System for Nucleic Acids Using Synthet
;  TITLE OF INVENTION:  Binding Systems
;  FILE REFERENCE: 264/217 Nanogen Recognomics
;  CURRENT APPLICATION NUMBER: US/09/910,469
;  CURRENT FILING DATE:  2001-07-19
;  NUMBER OF SEQ ID NOS: 184
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
;   LENGTH: 8
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic binding system
;   NAME/KEY: modified_base
;   LOCATION: (1)..(8)
;   OTHER INFORMATION: pyranosyl RNA
US-09-910-469-44

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 8;
  Best Local Similarity   80.0%;  Pred. No. 20;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          2 AGACT 6


RESULT 36
US-09-866-108A-9344
; Sequence 9344, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108A
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 15755
;  SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9344
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108A-9344

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 17;
  Best Local Similarity   80.0%;  Pred. No. 6.9;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          8 AGGCT 12


RESULT 37
US-09-866-108A-9345
; Sequence 9345, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108A
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
```

```
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 15755
;  SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9345
;    LENGTH: 17
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-09-866-108A-9345

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 17;
  Best Local Similarity   80.0%;  Pred. No. 6.9;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          7 AGGCT 11


RESULT 38
US-09-866-108A-9346
; Sequence 9346, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108A
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 15755
;  SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9346
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108A-9346

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 17;
  Best Local Similarity   80.0%;  Pred. No. 6.9;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          6 AGGCT 10


RESULT 39
US-08-859-954-566
; Sequence 566, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  566:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-566

  Query Match             15.0%;  Score 3;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTG 3
              |||
Db          1 TTG 3
```

```
RESULT 40
US-08-701-270-9/c
; Sequence 9, Application US/08701270
; Patent No. 5702926
;  GENERAL INFORMATION:
;    APPLICANT:  Fraiser, Melinda S.
;    APPLICANT:  Walker, George T.
;    TITLE OF INVENTION:  STRAND DISPLACEMENT AMPLIFICATION USING
;    TITLE OF INVENTION:  BORONATED NUCLEOTIDES
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Richard J. Rodrick, Becton Dickinson and
;      ADDRESSEE:  Company
;      STREET:  1 Becton Drive
;      CITY:  Franklin Lakes
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07417
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/701,270
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fugit, Donna R.
;      REGISTRATION NUMBER:  32,135
;      REFERENCE/DOCKET NUMBER:  P-3556
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-701-270-9

  Query Match             15.0%;  Score 3;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTG 3
              |||
Db          8 TTG 6


RESULT 41
US-08-859-954-501
; Sequence 501, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  501:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-501

  Query Match             14.0%;  Score 2.8;  DB 1;  Length 8;
  Best Local Similarity   66.7%;  Pred. No. 20;
  Matches    4;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CTCCAG 10
              ||  ||
Db          2 CTGGAG 7


RESULT 42
US-08-859-954-75
; Sequence 75, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  75:
```

```
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-75

  Query Match             12.0%;  Score 2.4;  DB 1;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 20;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTC 12
              || |
Db          3 AGAC 6


RESULT 43
US-08-859-954-264
; Sequence 264, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  264:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-264

  Query Match             12.0%;  Score 2.4;  DB 1;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 20;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTC 12
              || |
Db          5 AGAC 8


RESULT 44
US-08-859-954-44/c
; Sequence 44, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  44:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-44

  Query Match             12.0%;  Score 2.4;  DB 1;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 20;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTC 12
              || |
Db          5 AGAC 2


RESULT 45
US-08-859-954-74
; Sequence 74, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
```

```
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  74:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-74

  Query Match             12.0%;  Score 2.4;  DB 1;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 20;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTC 12
              || |
Db          3 AGAC 6


RESULT 46
US-08-859-954-401
; Sequence 401, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  401:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-401

  Query Match             12.0%;  Score 2.4;  DB 1;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 20;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTC 12
              || |
Db          5 AGAC 8


RESULT 47
US-08-859-954-263
; Sequence 263, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  263:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
```

```
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-263

  Query Match             10.0%;  Score 2;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 AG 10
              ||
Db          3 AG 4


RESULT 48
US-09-579-536C-43
; Sequence 43, Application US/09579536C
; Patent No. 6716974
; GENERAL INFORMATION:
;  APPLICANT: MACIAG, Thomas
;  APPLICANT:  ZIMRIN, Ann
;  APPLICANT:  SMALL, Deena
;  APPLICANT:  PRUDOVSKY, Igor
;  TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC METHODS AND COMPOSITIONS BASED ON JAGG
;  TITLE OF INVENTION:  PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE: 053689-5002-01
;  CURRENT APPLICATION NUMBER: US/09/579,536C
;  CURRENT FILING DATE:  2000-05-24
;  PRIOR APPLICATION NUMBER: US 09/199,865
;  PRIOR FILING DATE: 1998-11-25
;  PRIOR APPLICATION NUMBER: PCT/US97/09407
;  PRIOR FILING DATE: 1997-05-30
;  PRIOR APPLICATION NUMBER: US 60/018,841
;  PRIOR FILING DATE: 1996-05-31
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-579-536C-43

  Query Match             10.0%;  Score 2;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 AG 10
              ||
Db          2 AG 3


Search completed: April 23, 2006, 11:44:45
Job time : 1 secs
```

THIS PAGE LEFT BLANK

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 23, 2006, 11:37:56 ; Search time 0.001 Seconds
(without alignments)
19.200 Million cell updates/sec

Title: US-10-728-399-1
Perfect score: 20
Sequence: 1 ttgtctccagtctcttcgtt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 44 seqs, 480 residues

Total number of hits satisfying chosen parameters: 88

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : rge.subdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	13.8	69.0	17	1	CQ624604	ACCESSION:CQ624604
c	2	13.8	69.0	17	1	CQ624605	ACCESSION:CQ624605
c	3	13.8	69.0	17	1	CQ624606	ACCESSION:CQ624606
c	4	13.8	69.0	17	1	AR465667	ACCESSION:AR465667
c	5	13.8	69.0	17	1	AR465668	ACCESSION:AR465668
c	6	13.8	69.0	17	1	AR465669	ACCESSION:AR465669
c	7	9.4	47.0	11	1	CQ835687	ACCESSION:CQ835687
c	8	9.4	47.0	11	1	CQ836521	ACCESSION:CQ836521
c	9	9.4	47.0	11	1	AX624946	ACCESSION:AX624946
c	10	9.4	47.0	11	1	AX632367	ACCESSION:AX632367
c	11	9	45.0	11	1	AX471575	ACCESSION:AX471575
c	12	9	45.0	11	1	AX623703	ACCESSION:AX623703
c	13	9	45.0	11	1	AX626145	ACCESSION:AX626145
	14	9	45.0	11	1	AX626980	ACCESSION:AX626980
	15	9	45.0	11	1	AX629950	ACCESSION:AX629950
c	16	9	45.0	11	1	AX631124	ACCESSION:AX631124
c	17	9	45.0	11	1	AX924254	ACCESSION:AX924254
c	18	8.4	42.0	10	1	A04820	ACCESSION:A04820
c	19	8.4	42.0	10	1	BD239234	ACCESSION:BD239234
	20	8.4	42.0	10	1	I86909	ACCESSION:I86909
c	21	8.4	42.0	10	1	AR492617	ACCESSION:AR492617
c	22	8	40.0	10	1	A11620	ACCESSION:A11620
c	23	8	40.0	10	1	A35162	ACCESSION:A35162
	24	8	40.0	10	1	BD065278	ACCESSION:BD065278
	25	8	40.0	10	1	BD161225	ACCESSION:BD161225
c	26	8	40.0	10	1	BD161349	ACCESSION:BD161349
	27	8	40.0	10	1	CS101372	ACCESSION:CS101372
c	28	8	40.0	10	1	E27858	ACCESSION:E27858
	29	8	40.0	10	1	E39559	ACCESSION:E39559
c	30	8	40.0	10	1	AR306857	ACCESSION:AR306857
	31	8	40.0	10	1	AX152455	ACCESSION:AX152455
	32	8	40.0	10	1	AX152820	ACCESSION:AX152820
	33	8	40.0	10	1	AX301623	ACCESSION:AX301623
	34	8	40.0	10	1	AX301660	ACCESSION:AX301660
	35	7.4	37.0	9	1	CS133813	ACCESSION:CS133813
c	36	7.4	37.0	9	1	CS133814	ACCESSION:CS133814
	37	7.4	37.0	9	1	CS133839	ACCESSION:CS133839
	38	7.4	37.0	9	1	CS133878	ACCESSION:CS133878
	39	7.4	37.0	9	1	CS133889	ACCESSION:CS133889
c	40	7.4	37.0	9	1	CS133890	ACCESSION:CS133890
c	41	7.4	37.0	9	1	CS133996	ACCESSION:CS133996
	42	7	35.0	8	1	CQ787902	ACCESSION:CQ787902
	43	7	35.0	8	1	AX687122	ACCESSION:AX687122
c	44	7	35.0	8	1	AX687123	ACCESSION:AX687123
c	45	5	25.0	9	1	CS133878	ACCESSION:CS133878
	46	4.8	24.0	11	1	CQ835687	ACCESSION:CQ835687
c	47	4.4	22.0	9	1	CS133839	ACCESSION:CS133839
c	48	4.2	21.0	10	1	CS101372	ACCESSION:CS101372
	49	4.2	21.0	10	1	E27858	ACCESSION:E27858
	50	4.2	21.0	10	1	AR306857	ACCESSION:AR306857
c	51	4	20.0	11	1	AX629950	ACCESSION:AX629950
	52	3.8	19.0	10	1	A04820	ACCESSION:A04820
c	53	3.6	18.0	11	1	AX626980	ACCESSION:AX626980
c	54	3.4	17.0	8	1	AX687122	ACCESSION:AX687122
	55	3.4	17.0	8	1	AX687123	ACCESSION:AX687123
	56	3.4	17.0	9	1	CS133814	ACCESSION:CS133814
	57	3.4	17.0	10	1	BD161349	ACCESSION:BD161349
c	58	3.4	17.0	10	1	AX152820	ACCESSION:AX152820
c	59	3.4	17.0	10	1	AX301623	ACCESSION:AX301623
	60	3.4	17.0	11	1	AX624946	ACCESSION:AX624946
	61	3.4	17.0	11	1	AX632367	ACCESSION:AX632367
	62	3.4	17.0	11	1	AX471575	ACCESSION:AX471575
	63	3.4	17.0	11	1	AX626145	ACCESSION:AX626145
	64	3.4	17.0	17	1	CQ624604	ACCESSION:CQ624604
	65	3.4	17.0	17	1	CQ624605	ACCESSION:CQ624605
	66	3.4	17.0	17	1	CQ624606	ACCESSION:CQ624606
	67	3.4	17.0	17	1	AR465667	ACCESSION:AR465667
	68	3.4	17.0	17	1	AR465668	ACCESSION:AR465668
	69	3.4	17.0	17	1	AR465669	ACCESSION:AR465669
	70	3.2	16.0	10	1	BD239234	ACCESSION:BD239234
	71	3.2	16.0	11	1	AX623703	ACCESSION:AX623703
	72	3.2	16.0	11	1	AX631124	ACCESSION:AX631124
c	73	3	15.0	10	1	I86909	ACCESSION:I86909
c	74	2.8	14.0	10	1	BD065278	ACCESSION:BD065278
c	75	2.8	14.0	10	1	BD161225	ACCESSION:BD161225
c	76	2.8	14.0	10	1	E39559	ACCESSION:E39559
c	77	2.8	14.0	10	1	AX152455	ACCESSION:AX152455
c	78	2.8	14.0	10	1	AX301660	ACCESSION:AX301660
c	79	2.4	12.0	8	1	CQ787902	ACCESSION:CQ787902
c	80	2.4	12.0	9	1	CS133813	ACCESSION:CS133813
	81	2.4	12.0	9	1	CS133890	ACCESSION:CS133890
	82	2.4	12.0	9	1	CS133996	ACCESSION:CS133996
	83	2.4	12.0	10	1	A11620	ACCESSION:A11620
	84	2.4	12.0	10	1	A35162	ACCESSION:A35162
	85	2.2	11.0	11	1	CQ836521	ACCESSION:CQ836521
c	86	2	10.0	9	1	CS133889	ACCESSION:CS133889
	87	2	10.0	10	1	AR492617	ACCESSION:AR492617
	88	2	10.0	11	1	AX924254	ACCESSION:AX924254

ALIGNMENTS

RESULT 1
CQ624604/c
LOCUS CQ624604 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 9344 from Patent WO0192524.
ACCESSION CQ624604
VERSION CQ624604.1 GI:41674822
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1

```
  AUTHORS   Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
  TITLE     Myosin-like gene expressed in human heart and muscle
  JOURNAL   Patent: WO 0192524-A 9344 06-DEC-2001;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             69.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.5;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 TCTCCAGTCTCTTCGTT 20
              || |||| |||||||||
Db         17 TCCCCAGCCTCTTCGTT 1


RESULT 2
CQ624605/c
LOCUS       CQ624605                  17 bp    DNA     linear   PAT 02-FEB-2004
DEFINITION  Sequence 9345 from Patent WO0192524.
ACCESSION   CQ624605
VERSION     CQ624605.1  GI:41674823
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
  TITLE     Myosin-like gene expressed in human heart and muscle
  JOURNAL   Patent: WO 0192524-A 9345 06-DEC-2001;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             69.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.5;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAGTCTCTTCGT 19
              ||| |||| ||||||||
Db         17 GTCCCCAGCCTCTTCGT 1


RESULT 3
CQ624606/c
LOCUS       CQ624606                  17 bp    DNA     linear   PAT 02-FEB-2004
DEFINITION  Sequence 9346 from Patent WO0192524.
ACCESSION   CQ624606
VERSION     CQ624606.1  GI:41674824
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
  TITLE     Myosin-like gene expressed in human heart and muscle
  JOURNAL   Patent: WO 0192524-A 9346 06-DEC-2001;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             69.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.5;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TGTCTCCAGTCTCTTCG 18
              |||| |||| |||||||
Db         17 TGTCCCCAGCCTCTTCG 1


RESULT 4
AR465667/c
LOCUS       AR465667                  17 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 9344 from patent US 6686188.
ACCESSION   AR465667
VERSION     AR465667.1  GI:42700724
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
  TITLE     Polynucleotide encoding a human myosin-like polypeptide expressed
            predominantly in heart and muscle
  JOURNAL   Patent: US 6686188-A 9344 03-FEB-2004;
            Amersham PLC; Buckinghamshire;
            GBX;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             69.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.5;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 TCTCCAGTCTCTTCGTT 20
              || |||| |||||||||
Db         17 TCCCCAGCCTCTTCGTT 1


RESULT 5
AR465668/c
LOCUS       AR465668                  17 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 9345 from patent US 6686188.
ACCESSION   AR465668
VERSION     AR465668.1  GI:42700725
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
  TITLE     Polynucleotide encoding a human myosin-like polypeptide expressed
            predominantly in heart and muscle
  JOURNAL   Patent: US 6686188-A 9345 03-FEB-2004;
            Amersham PLC; Buckinghamshire;
            GBX;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             69.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.5;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAGTCTCTTCGT 19
```

```
            ||| |||| ||||||||
Db         17 GTCCCCAGCCTCTTCGT 1


RESULT 6
AR465669/c
LOCUS       AR465669                  17 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 9346 from patent US 6686188.
ACCESSION   AR465669
VERSION     AR465669.1  GI:42700726
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
  TITLE     Polynucleotide encoding a human myosin-like polypeptide expressed
            predominantly in heart and muscle
  JOURNAL   Patent: US 6686188-A 9346 03-FEB-2004;
            Amersham PLC; Buckinghamshire;
            GBX;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             69.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.5;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TGTCTCCAGTCTCTTCG 18
            |||| |||| |||||||
Db         17 TGTCCCCAGCCTCTTCG 1


RESULT 7
CQ835687/c
LOCUS       CQ835687                  11 bp    DNA     linear   PAT 29-JUL-2004
DEFINITION  Sequence 745 from Patent WO2004059001.
ACCESSION   CQ835687
VERSION     CQ835687.1  GI:50835221
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
  TITLE     Method for determining markers of human facial skin
  JOURNAL   Patent: WO 2004059001-A 745 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 11;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TTGTCTCCAGT 11
              |||||| ||||
Db         11 TTGTCTGCAGT 1


RESULT 8
CQ836521/c
LOCUS       CQ836521                  11 bp    DNA     linear   PAT 29-JUL-2004
DEFINITION  Sequence 1579 from Patent WO2004059001.
ACCESSION   CQ836521
VERSION     CQ836521.1  GI:50836055
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
  TITLE     Method for determining markers of human facial skin
  JOURNAL   Patent: WO 2004059001-A 1579 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 11;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 CCAGTCTCTTC 17
              ||||| |||||
Db         11 CCAGTTTCTTC 1


RESULT 9
AX624946/c
LOCUS       AX624946                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 1987 from Patent WO02053774.
ACCESSION   AX624946
VERSION     AX624946.1  GI:28452887
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 1987 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 11;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 CCAGTCTCTTC 17
              |||| ||||||
Db         11 CCAGCCTCTTC 1


RESULT 10
AX632367/c
LOCUS       AX632367                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 9409 from Patent WO02053774.
ACCESSION   AX632367
VERSION     AX632367.1  GI:28467982
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
```

```
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 9409 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 11;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 CCAGTCTCTTC 17
              |||| ||||||
Db         11 CCAGCCTCTTC 1


RESULT 11
AX471575/c
LOCUS       AX471575                  11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 1152 from Patent WO02053773.
ACCESSION   AX471575
VERSION     AX471575.1  GI:22206700
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 1152 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 AGTCTCTTC 17
              |||||||||
Db         10 AGTCTCTTC 2


RESULT 12
AX623703/c
LOCUS       AX623703                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 744 from Patent WO02053774.
ACCESSION   AX623703
VERSION     AX623703.1  GI:28451644
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 744 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TGTCTCCAG 10
              |||||||||
Db         11 TGTCTCCAG 3


RESULT 13
AX626145/c
LOCUS       AX626145                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 3186 from Patent WO02053774.
ACCESSION   AX626145
VERSION     AX626145.1  GI:28454183
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 3186 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 AGTCTCTTC 17
              |||||||||
Db         10 AGTCTCTTC 2


RESULT 14
AX626980
LOCUS       AX626980                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 4021 from Patent WO02053774.
ACCESSION   AX626980
VERSION     AX626980.1  GI:28455018
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 4021 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TGTCTCCAG 10
              |||||||||
Db          3 TGTCTCCAG 11
```

```
RESULT 15
AX629950
LOCUS       AX629950                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 6991 from Patent WO02053774.
ACCESSION   AX629950
VERSION     AX629950.1  GI:28457988
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 6991 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TGTCTCCAG 10
              |||||||||
Db          3 TGTCTCCAG 11


RESULT 16
AX631124/c
LOCUS       AX631124                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 8165 from Patent WO02053774.
ACCESSION   AX631124
VERSION     AX631124.1  GI:28459168
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 8165 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TGTCTCCAG 10
              |||||||||
Db         11 TGTCTCCAG 3


RESULT 17
AX924254/c
LOCUS       AX924254                  11 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 39 from Patent EP1350841.
ACCESSION   AX924254
VERSION     AX924254.1  GI:40217178
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Schoenbrunner,N.J., Myers,T.W. and Gelfland,D.H.
  TITLE     Thermostable or thermoactive DNA polymerase with attenuated
            3'-5'exonuclease activity
  JOURNAL   Patent: EP 1350841-A 39 08-OCT-2003;
            Roche Diagnostics GmbH (DE) ; F. HOFFMANN-LA ROCHE AG (CH)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          11 TCTCTTCGT 19
               |||||||||
Db          11 TCTCTTCGT 3


RESULT 18
A04820/c
LOCUS       A04820                    10 bp    DNA     linear   PAT 14-JUL-1993
DEFINITION  Nucleotide sequence 8 from patent number EP0143081.
ACCESSION   A04820
VERSION     A04820.1  GI:411098
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Meyhack,B. and Hinnen,A.
  TITLE     Synthesis of tissue plasminogen activator(TPA) by yeast
  JOURNAL   Patent: EP 0143081-A 8 29-MAY-1985;
            CIBA-GEIGY AG
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 CAGTCTCTTC 17
              |||| |||||
Db         10 CAGTGTCTTC 1


RESULT 19
BD239234/c
LOCUS       BD239234                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD239234
VERSION     BD239234.1  GI:33049004
KEYWORDS    JP 2002534056-A/652.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 652 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/652
```

```
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
            19-JUN-1998 US    60/090080,19-JUN-1998 US    60/089833 PR
            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TGTCTCCAGT 11
              || |||||||
Db         10 TGGCTCCAGT 1


RESULT 20
I86909
LOCUS       I86909                   10 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 9 from patent US 5702926.
ACCESSION   I86909
VERSION     I86909.1  GI:3206627
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Fraiser,M.S. and Walker,G.Terrance.
  TITLE     Nicking of DNA using boronated nucleotides
  JOURNAL   Patent: US 5702926-A 9 30-DEC-1997;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAGTC 12
              ||||||| ||
Db          1 GTCTCCAATC 10


RESULT 21
AR492617/c
LOCUS       AR492617                 10 bp    DNA     linear   PAT 15-MAY-2004
DEFINITION  Sequence 43 from patent US 6716974.
ACCESSION   AR492617
VERSION     AR492617.1  GI:47262128
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Maciag,T., Zimrin,A.B., Small,D.J. and Prudovsky,I.A.
  TITLE     Therapeutic and diagnostic methods and compositions based on
            jagged/notch proteins and nucleic acids
  JOURNAL   Patent: US 6716974-A 43 06-APR-2004;
            Maine Medical Center Research Institute; Scarborough, ME
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 TCTCTTCGTT 20
              ||||||| ||
Db         10 TCTCTTCCTT 1


RESULT 22
A11620/c
LOCUS       A11620                   10 bp    DNA     linear   PAT 17-NOV-1993
DEFINITION  oligonucleotide 'M''.
ACCESSION   A11620
VERSION     A11620.1  GI:489366
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Ueda,I., Niwa,M., Saito,Y., Sato,S., Ono,H. and Kitaguchi,T.
  TITLE     59 Valine insulin-like growth factor I and process for production
            thereof
  JOURNAL   Patent: EP 0158892-A 116 23-OCT-1985;
            FUJISAWA PHARMACEUTICAL CO., LTD
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTGTCTCC 8
              ||||||||
Db          8 TTGTCTCC 1


RESULT 23
A35162/c
LOCUS       A35162                   10 bp    DNA     linear   PAT 06-DEC-1996
DEFINITION  Synthetic IGF-I gene oligo.
ACCESSION   A35162
VERSION     A35162.1  GI:1926821
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Ueda,I., Niwa,M., Satoh,S., Saitoh,Y. and Kusunoki,C.
  TITLE     Process for production of isulin-like growth factor I and plasmid
            for production thereof
  JOURNAL   Patent: EP 0219814-A 112 29-APR-1987;
```

```
            FUJISAWA PHARMACEUTICAL CO., LTD
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTGTCTCC 8
              ||||||||
Db          8 TTGTCTCC 1


RESULT 24
BD065278
LOCUS       BD065278                  10 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Characterization of the yeast transcriptome.
ACCESSION   BD065278
VERSION     BD065278.1  GI:22610881
KEYWORDS    JP 2001509017-A/214.
SOURCE      Saccharomyces cerevisiae (baker's yeast)
  ORGANISM  Saccharomyces cerevisiae
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Characterization of the yeast transcriptome
  JOURNAL   Patent: JP 2001509017-A 214 10-JUL-2001;
            THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
COMMENT     OS   Saccharomyces cerevisiae (yeast)
            PN   JP 2001509017-A/214
            PD   10-JUL-2001
            PF   22-JAN-1998 JP 1998532117
            PR   23-JAN-1997 US    60/035917
            PI   VICTOR E VELCULESCU,BERT VOGELSTEIN,KENNETH W KINZLER PC
           C12N15/10,C12N15/31,C07K14/395,C12Q1/68,C12Q1/02 CC
            Characterization of the yeast transcriptome
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Saccharomyces cerevisiae (yeast)'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Saccharomyces cerevisiae"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:4932"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TCTCCAGT 11
              ||||||||
Db          1 TCTCCAGT 8


RESULT 25
BD161225
LOCUS       BD161225                  10 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Human activated Th1 and Th2 cell expression genes.
ACCESSION   BD161225
VERSION     BD161225.1  GI:27866983
KEYWORDS    JP 2002186482-A/47.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Nagai,S., Matsushima,K. and Hashimoto,S.
  TITLE     Human activated Th1 and Th2 cell expression genes
  JOURNAL   Patent: JP 2002186482-A 47 02-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002186482-A/47
            PD   02-JUL-2002
            PF   19-DEC-2000 JP 2000385816
            PI   SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
            C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC   Human
            activated Th1 and Th2 cell expression genes FH   Key
            Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TCTCCAGT 11
              ||||||||
Db          3 TCTCCAGT 10


RESULT 26
BD161349/c
LOCUS       BD161349                  10 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Human activated Th1 and Th2 cell expression genes.
ACCESSION   BD161349
VERSION     BD161349.1  GI:27867107
KEYWORDS    JP 2002186482-A/171.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Nagai,S., Matsushima,K. and Hashimoto,S.
  TITLE     Human activated Th1 and Th2 cell expression genes
  JOURNAL   Patent: JP 2002186482-A 171 02-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002186482-A/171
            PD   02-JUL-2002
            PF   19-DEC-2000 JP 2000385816
            PI   SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
            C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC   Human
            activated Th1 and Th2 cell expression genes FH   Key
            Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 TCCAGTCT 13
              ||||||||
Db          8 TCCAGTCT 1


RESULT 27
CS101372
LOCUS       CS101372                  10 bp    DNA     linear   PAT 10-JUN-2005
DEFINITION  Sequence 21 from Patent WO2005045021.
```

```
ACCESSION   CS101372
VERSION     CS101372.1  GI:67509818
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Desire,L.
  TITLE     Bace455, an alternative splice variant of the human beta-secretase
  JOURNAL   Patent: WO 2005045021-A 21 19-MAY-2005;
            Exonhit Therapeutics S.A. (FR)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="primer"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CAGTCTCT 15
              ||||||||
Db          1 CAGTCTCT 8


RESULT 28
E27858/c
LOCUS       E27858                    10 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for testing resistance of rice against Nilaparvata lugens
            Stal, DNA fragment and PCR marker.
ACCESSION   E27858
VERSION     E27858.1  GI:13018283
KEYWORDS    JP 1999206376-A/9.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Takamichi,T., Hitoshi,N., Takako,T. and Norikuni,S.
  TITLE     Method for testing resistance of rice against Nilaparvata lugens
            Stal, DNA fragment and PCR marker
  JOURNAL   Patent: JP 1999206376-A 9 03-AUG-1999;
            AICHI PREF
COMMENT     OS   Unidentified
            PN   JP 1999206376-A/9
            PD   03-AUG-1999
            PF   22-JAN-1998 JP 1998010845
            PR
            PI   TAKAMICHI TOYAMA,HITOSHI NAKAMAE,TAKAKO TSUJI,NORIKUNI SAKA PC
              C12N15/09,C12Q1/68,G01N33/50//(C12N15/09,C12R1:91),C12N15/00, PC
             (C12N15/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAG 10
              ||||||||
Db         10 GTCTCCAG 3


RESULT 29
E39559
LOCUS       E39559                    10 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Genes with human dendritic cell expression.
ACCESSION   E39559
VERSION     E39559.1  GI:18621650
KEYWORDS    JP 2000279181-A/92.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Hashimoto,S., Matsushima,K. and Suzuki,T.
  TITLE     Genes with human dendritic cell expression
  JOURNAL   Patent: JP 2000279181-A 92 10-OCT-2000;
            SCIENCE & TECH AGENCY
COMMENT     OS   Homo sapiens (human)
            PN   JP 2000279181-A/92
            PD   10-OCT-2000
            PF   01-APR-1999 JP 1999095481
            PR
            PI   SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
            C12N15/09,C07K14/475,C07K16/18,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TCTCCAGT 11
              ||||||||
Db          3 TCTCCAGT 10


RESULT 30
AR306857/c
LOCUS       AR306857                  10 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 9 from patent US 6551476.
ACCESSION   AR306857
VERSION     AR306857.1  GI:31697257
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Scherba,E.S.
  TITLE     Noble-metal coated inert anode for aluminum production
  JOURNAL   Patent: US 6551476-A 9 22-APR-2003;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CTCCAGTC 12
              ||||||||
Db          9 CTCCAGTC 2


RESULT 31
AX152455
LOCUS       AX152455                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 370 from Patent WO0138577.
```

```
ACCESSION   AX152455
VERSION     AX152455.1  GI:14534106
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 370 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TCTCCAGT 11
              ||||||||
Db          3 TCTCCAGT 10


RESULT 32
AX152820
LOCUS       AX152820                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 735 from Patent WO0138577.
ACCESSION   AX152820
VERSION     AX152820.1  GI:14534471
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 735 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CAGTCTCT 15
              ||||||||
Db          1 CAGTCTCT 8


RESULT 33
AX301623
LOCUS       AX301623                  10 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 337 from Patent WO0185941.
ACCESSION   AX301623
VERSION     AX301623.1  GI:17382706
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Versteeg,R. and Caron,H.N.
  TITLE     Myc targets
  JOURNAL   Patent: WO 0185941-A 337 15-NOV-2001;
            Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CAGTCTCT 15
              ||||||||
Db          1 CAGTCTCT 8


RESULT 34
AX301660
LOCUS       AX301660                  10 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 374 from Patent WO0185941.
ACCESSION   AX301660
VERSION     AX301660.1  GI:17382743
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Versteeg,R. and Caron,H.N.
  TITLE     Myc targets
  JOURNAL   Patent: WO 0185941-A 374 15-NOV-2001;
            Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TCTCCAGT 11
              ||||||||
Db          3 TCTCCAGT 10


RESULT 35
CS133813
LOCUS       CS133813                   9 bp    DNA     linear   PAT 02-AUG-2005
DEFINITION  Sequence 355 from Patent WO2005058479.
ACCESSION   CS133813
VERSION     CS133813.1  GI:71793362
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Morgan,B.
  TITLE     Methods for synthesis of encoded libraries
  JOURNAL   Patent: WO 2005058479-A 355 30-JUN-2005;
            Praecis Pharmaceuticals Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic construct"
```

```
  Query Match            37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 87;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 TCTCTTCGT 19
              |||| ||||
Db          1 TCTCCTCGT 9


RESULT 36
CS133814/c
LOCUS       CS133814                  9 bp    DNA     linear   PAT 02-AUG-2005
DEFINITION  Sequence 356 from Patent WO2005058479.
ACCESSION   CS133814
VERSION     CS133814.1  GI:71793363
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Morgan,B.
  TITLE     Methods for synthesis of encoded libraries
  JOURNAL   Patent: WO 2005058479-A 356 30-JUN-2005;
            Praecis Pharmaceuticals Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic construct"

  Query Match            37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 87;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCTCTTC 17
              |||||| ||
Db          9 AGTCTCCTC 1


RESULT 37
CS133839
LOCUS       CS133839                  9 bp    DNA     linear   PAT 02-AUG-2005
DEFINITION  Sequence 381 from Patent WO2005058479.
ACCESSION   CS133839
VERSION     CS133839.1  GI:71793388
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Morgan,B.
  TITLE     Methods for synthesis of encoded libraries
  JOURNAL   Patent: WO 2005058479-A 381 30-JUN-2005;
            Praecis Pharmaceuticals Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic construct"

  Query Match            37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 87;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 CCAGTCTCT 15
              ||||||| |
Db          1 CCAGTCTGT 9


RESULT 38
CS133878
LOCUS       CS133878                  9 bp    DNA     linear   PAT 02-AUG-2005
DEFINITION  Sequence 420 from Patent WO2005058479.
ACCESSION   CS133878
VERSION     CS133878.1  GI:71793427
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Morgan,B.
  TITLE     Methods for synthesis of encoded libraries
  JOURNAL   Patent: WO 2005058479-A 420 30-JUN-2005;
            Praecis Pharmaceuticals Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic construct"

  Query Match            37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 87;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 CTCCAGTCT 13
              |||||| ||
Db          1 CTCCAGACT 9


RESULT 39
CS133889
LOCUS       CS133889                  9 bp    DNA     linear   PAT 02-AUG-2005
DEFINITION  Sequence 431 from Patent WO2005058479.
ACCESSION   CS133889
VERSION     CS133889.1  GI:71793438
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Morgan,B.
  TITLE     Methods for synthesis of encoded libraries
  JOURNAL   Patent: WO 2005058479-A 431 30-JUN-2005;
            Praecis Pharmaceuticals Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic construct"

  Query Match            37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 87;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 TCTCTTCGT 19
              || ||||||
Db          1 TCGCTTCGT 9


RESULT 40
CS133890/c
LOCUS       CS133890                  9 bp    DNA     linear   PAT 02-AUG-2005
DEFINITION  Sequence 432 from Patent WO2005058479.
ACCESSION   CS133890
VERSION     CS133890.1  GI:71793439
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Morgan,B.
  TITLE     Methods for synthesis of encoded libraries
```

```
  JOURNAL   Patent: WO 2005058479-A 432 30-JUN-2005;
            Praecis Pharmaceuticals Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic construct"

  Query Match            37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity  88.9%;  Pred. No. 87;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCTCTTC 17
              |||| ||||
Db          9 AGTCGCTTC 1


RESULT 41
CS133996/c
LOCUS       CS133996                  9 bp    DNA     linear   PAT 02-AUG-2005
DEFINITION  Sequence 538 from Patent WO2005058479.
ACCESSION   CS133996
VERSION     CS133996.1  GI:71793545
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Morgan,B.
  TITLE     Methods for synthesis of encoded libraries
  JOURNAL   Patent: WO 2005058479-A 538 30-JUN-2005;
            Praecis Pharmaceuticals Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic construct"

  Query Match            37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity  88.9%;  Pred. No. 87;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 GTCTCTTCG 18
              ||||| |||
Db          9 GTCTCCTCG 1


RESULT 42
CQ787902
LOCUS       CQ787902                  8 bp    DNA     linear   PAT 24-MAR-2004
DEFINITION  Sequence 208 from Patent WO2004020664.
ACCESSION   CQ787902
VERSION     CQ787902.1  GI:45722860
KEYWORDS    .
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1
  AUTHORS   Geldermann,H., Preuss,S. and Han,Y.
  TITLE     Polymorphous microsatellite loci in genes for pre-diagnostic
            purposes
  JOURNAL   Patent: WO 2004020664-A 208 11-MAR-2004;
            Universitaet Hohenheim (DE)
FEATURES             Location/Qualifiers
     source          1. .8
                     /organism="Bos taurus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9913"
     satellite       1. .8
                     /note="R16, Allel H"
     repeat_unit     1
                     /note="Anzahl der Wiederholungen: 4"
     repeat_unit     3
                     /note="Anzahl der Wiederholungen: 13"
     repeat_unit     5
                     /note="Anzahl der Wiederholungen: 3"
     repeat_unit     8
                     /note="Anzahl der Wiederholungen: 4"

  Query Match            35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 98;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TGTCTCC 8
              |||||||
Db          1 TGTCTCC 7


RESULT 43
AX687122
LOCUS       AX687122                  8 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 43 from Patent WO03008638.
ACCESSION   AX687122
VERSION     AX687122.1  GI:29409617
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Schweitzer,M., Anderson,R., Fiechtner,M., Mueller-Ibeler,J.,
            Raddatz,S., Bruecher,C., Windhab,N., Orwick,J., Schneider,E.,
            Pignot,M. and Kienle,S.
  TITLE     Sorting and immobilization system for nucleic acids using synthetic
            binding systems
  JOURNAL   Patent: WO 03008638-A 43 30-JAN-2003;
            Nanogen Recognomics GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .8
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic binding system"
     misc_feature    1. .8
                     /note="pyranosyl RNA"

  Query Match            35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 98;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CCAGTCT 13
              |||||||
Db          1 CCAGTCT 7


RESULT 44
AX687123/c
LOCUS       AX687123                  8 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 44 from Patent WO03008638.
ACCESSION   AX687123
VERSION     AX687123.1  GI:29409618
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Schweitzer,M., Anderson,R., Fiechtner,M., Mueller-Ibeler,J.,
            Raddatz,S., Bruecher,C., Windhab,N., Orwick,J., Schneider,E.,
            Pignot,M. and Kienle,S.
  TITLE     Sorting and immobilization system for nucleic acids using synthetic
            binding systems
  JOURNAL   Patent: WO 03008638-A 44 30-JAN-2003;
            Nanogen Recognomics GmbH (DE)
```

```
FEATURES             Location/Qualifiers
     source          1. .8
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic binding system"
     misc_feature    1. .8
                     /note="pyranosyl RNA"

  Query Match           35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 98;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CCAGTCT 13
              |||||||
Db          8 CCAGTCT 2


RESULT 45
CS133878/c
LOCUS       CS133878                  9 bp    DNA     linear   PAT 02-AUG-2005
DEFINITION  Sequence 420 from Patent WO2005058479.
ACCESSION   CS133878
VERSION     CS133878.1  GI:71793427
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Morgan,B.
  TITLE     Methods for synthesis of encoded libraries
  JOURNAL   Patent: WO 2005058479-A 420 30-JUN-2005;
            Praecis Pharmaceuticals Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic construct"

  Query Match           25.0%;  Score 5;  DB 1;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 87;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              |||||
Db          9 AGTCT 5


RESULT 46
CQ835687
LOCUS       CQ835687                 11 bp    DNA     linear   PAT 29-JUL-2004
DEFINITION  Sequence 745 from Patent WO2004059001.
ACCESSION   CQ835687
VERSION     CQ835687.1  GI:50835221
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
  TITLE     Method for determining markers of human facial skin
  JOURNAL   Patent: WO 2004059001-A 745 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match           24.0%;  Score 4.8;  DB 1;  Length 11;
  Best Local Similarity  75.0%;  Pred. No. 42;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CTCCAGTC 12
              || ||| |
Db          2 CTGCAGAC 9


RESULT 47
CS133839/c
LOCUS       CS133839                  9 bp    DNA     linear   PAT 02-AUG-2005
DEFINITION  Sequence 381 from Patent WO2005058479.
ACCESSION   CS133839
VERSION     CS133839.1  GI:71793388
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Morgan,B.
  TITLE     Methods for synthesis of encoded libraries
  JOURNAL   Patent: WO 2005058479-A 381 30-JUN-2005;
            Praecis Pharmaceuticals Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic construct"

  Query Match           22.0%;  Score 4.4;  DB 1;  Length 9;
  Best Local Similarity  83.3%;  Pred. No. 87;
  Matches    5;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 CAGTCT 13
              ||| ||
Db          8 CAGACT 3


RESULT 48
CS101372/c
LOCUS       CS101372                 10 bp    DNA     linear   PAT 10-JUN-2005
DEFINITION  Sequence 21 from Patent WO2005045021.
ACCESSION   CS101372
VERSION     CS101372.1  GI:67509818
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Desire,L.
  TITLE     Bace455, an alternative splice variant of the human beta-secretase
  JOURNAL   Patent: WO 2005045021-A 21 19-MAY-2005;
            Exonhit Therapeutics S.A. (FR)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="primer"

  Query Match           21.0%;  Score 4.2;  DB 1;  Length 10;
  Best Local Similarity  66.7%;  Pred. No. 53;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          7 CCAGTCTCT 15
              ||||   ||
Db         10 CCAGAGACT 2


RESULT 49
E27858
```

```
LOCUS       E27858                    10 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for testing resistance of rice against Nilaparvata lugens
            Stal, DNA fragment and PCR marker.
ACCESSION   E27858
VERSION     E27858.1  GI:13018283
KEYWORDS    JP 1999206376-A/9.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Takamichi,T., Hitoshi,N., Takako,T. and Norikuni,S.
  TITLE     Method for testing resistance of rice against Nilaparvata lugens
            Stal, DNA fragment and PCR marker
  JOURNAL   Patent: JP 1999206376-A 9 03-AUG-1999;
            AICHI PREF
COMMENT     OS   Unidentified
            PN   JP 1999206376-A/9
            PD   03-AUG-1999
            PF   22-JAN-1998 JP 1998010845
            PR
            PI   TAKAMICHI TOYAMA,HITOSHI NAKAMAE,TAKAKO TSUJI,NORIKUNI SAKA PC
              C12N15/09,C12Q1/68,G01N33/50//(C12N15/09,C12R1:91),C12N15/00, PC
             (C12N15/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             21.0%;  Score 4.2;  DB 1;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 53;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 TCTCCAGTC 12
              |||  || |
Db          2 TCTGGAGAC 10


RESULT 50
AR306857
LOCUS       AR306857                  10 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 9 from patent US 6551476.
ACCESSION   AR306857
VERSION     AR306857.1  GI:31697257
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Scherba,E.S.
  TITLE     Noble-metal coated inert anode for aluminum production
  JOURNAL   Patent: US 6551476-A 9 22-APR-2003;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             21.0%;  Score 4.2;  DB 1;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 53;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAGT 11
              | ||  |||
Db          2 GACTGGAGT 10


RESULT 51
AX629950/c
LOCUS       AX629950                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 6991 from Patent WO02053774.
ACCESSION   AX629950
VERSION     AX629950.1  GI:28457988
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 6991 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             20.0%;  Score 4;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CAGT 11
              ||||
Db          4 CAGT 1


RESULT 52
A04820
LOCUS       A04820                    10 bp    DNA     linear   PAT 14-JUL-1993
DEFINITION  Nucleotide sequence 8 from patent number EP0143081.
ACCESSION   A04820
VERSION     A04820.1  GI:411098
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Meyhack,B. and Hinnen,A.
  TITLE     Synthesis of tissue plasminogen activator(TPA) by yeast
  JOURNAL   Patent: EP 0143081-A 8 29-MAY-1985;
            CIBA-GEIGY AG
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             19.0%;  Score 3.8;  DB 1;  Length 10;
  Best Local Similarity   71.4%;  Pred. No. 57;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          9 AGTCTCT 15
              || | ||
Db          3 AGACACT 9


RESULT 53
AX626980/c
LOCUS       AX626980                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 4021 from Patent WO02053774.
ACCESSION   AX626980
VERSION     AX626980.1  GI:28455018
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
```

```
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 4021 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match           18.0%;  Score 3.6;  DB 1;  Length 11;
  Best Local Similarity   60.0%;  Pred. No. 54;
  Matches    6;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          5 CTCCAGTCTC 14
              ||  || | |
Db         11 CTGGAGACAC 2


RESULT 54
AX687122/c
LOCUS       AX687122                  8 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 43 from Patent WO03008638.
ACCESSION   AX687122
VERSION     AX687122.1  GI:29409617
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Schweitzer,M., Anderson,R., Fiechtner,M., Mueller-Ibeler,J.,
            Raddatz,S., Bruecher,C., Windhab,N., Orwick,J., Schneider,E.,
            Pignot,M. and Kienle,S.
  TITLE     Sorting and immobilization system for nucleic acids using synthetic
            binding systems
  JOURNAL   Patent: WO 03008638-A 43 30-JAN-2003;
            Nanogen Recognomics GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .8
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic binding system"
     misc_feature    1. .8
                     /note="pyranosyl RNA"

  Query Match           17.0%;  Score 3.4;  DB 1;  Length 8;
  Best Local Similarity   80.0%;  Pred. No. 98;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          7 AGACT 3


RESULT 55
AX687123
LOCUS       AX687123                  8 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 44 from Patent WO03008638.
ACCESSION   AX687123
VERSION     AX687123.1  GI:29409618
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Schweitzer,M., Anderson,R., Fiechtner,M., Mueller-Ibeler,J.,
            Raddatz,S., Bruecher,C., Windhab,N., Orwick,J., Schneider,E.,
            Pignot,M. and Kienle,S.
  TITLE     Sorting and immobilization system for nucleic acids using synthetic
            binding systems
  JOURNAL   Patent: WO 03008638-A 44 30-JAN-2003;
            Nanogen Recognomics GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .8
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic binding system"
     misc_feature    1. .8
                     /note="pyranosyl RNA"

  Query Match           17.0%;  Score 3.4;  DB 1;  Length 8;
  Best Local Similarity   80.0%;  Pred. No. 98;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          2 AGACT 6


RESULT 56
CS133814
LOCUS       CS133814                  9 bp    DNA     linear   PAT 02-AUG-2005
DEFINITION  Sequence 356 from Patent WO2005058479.
ACCESSION   CS133814
VERSION     CS133814.1  GI:71793363
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Morgan,B.
  TITLE     Methods for synthesis of encoded libraries
  JOURNAL   Patent: WO 2005058479-A 356 30-JUN-2005;
            Praecis Pharmaceuticals Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic construct"

  Query Match           17.0%;  Score 3.4;  DB 1;  Length 9;
  Best Local Similarity   80.0%;  Pred. No. 87;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          5 AGACT 9


RESULT 57
BD161349
LOCUS       BD161349                 10 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Human activated Th1 and Th2 cell expression genes.
ACCESSION   BD161349
VERSION     BD161349.1  GI:27867107
KEYWORDS    JP 2002186482-A/171.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Nagai,S., Matsushima,K. and Hashimoto,S.
  TITLE     Human activated Th1 and Th2 cell expression genes
  JOURNAL   Patent: JP 2002186482-A 171 02-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002186482-A/171
            PD   02-JUL-2002
            PF   19-DEC-2000 JP 2000385816
            PI   SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
            C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC   Human
            activated Th1 and Th2 cell expression genes FH   Key
            Location/Qualifiers
```

```
           FT   source          1. .10
           FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 61;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          1 AGACT 5


RESULT 58
AX152820/c
LOCUS       AX152820                10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 735 from Patent WO0138577.
ACCESSION   AX152820
VERSION     AX152820.1  GI:14534471
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 735 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 61;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          6 AGACT 2


RESULT 59
AX301623/c
LOCUS       AX301623                10 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 337 from Patent WO0185941.
ACCESSION   AX301623
VERSION     AX301623.1  GI:17382706
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Versteeg,R. and Caron,H.N.
  TITLE     Myc targets
  JOURNAL   Patent: WO 0185941-A 337 15-NOV-2001;
            Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 61;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          6 AGACT 2


RESULT 60
AX624946
LOCUS       AX624946                11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 1987 from Patent WO02053774.
ACCESSION   AX624946
VERSION     AX624946.1  GI:28452887
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 1987 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 11;
  Best Local Similarity   80.0%;  Pred. No. 56;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          5 AGGCT 9


RESULT 61
AX632367
LOCUS       AX632367                11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 9409 from Patent WO02053774.
ACCESSION   AX632367
VERSION     AX632367.1  GI:28467982
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 9409 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 11;
  Best Local Similarity   80.0%;  Pred. No. 56;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          5 AGGCT 9


RESULT 62
```

```
AX471575
LOCUS       AX471575                  11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 1152 from Patent WO02053773.
ACCESSION   AX471575
VERSION     AX471575.1  GI:22206700
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 1152 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 11;
  Best Local Similarity   80.0%;  Pred. No. 56;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          6 AGACT 10


RESULT 63
AX626145
LOCUS       AX626145                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 3186 from Patent WO02053774.
ACCESSION   AX626145
VERSION     AX626145.1  GI:28454183
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 3186 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 11;
  Best Local Similarity   80.0%;  Pred. No. 56;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          6 AGACT 10


RESULT 64
CQ624604
LOCUS       CQ624604                  17 bp    DNA     linear   PAT 02-FEB-2004
DEFINITION  Sequence 9344 from Patent WO0192524.
ACCESSION   CQ624604
VERSION     CQ624604.1  GI:41674822
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
  TITLE     Myosin-like gene expressed in human heart and muscle
  JOURNAL   Patent: WO 0192524-A 9344 06-DEC-2001;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 17;
  Best Local Similarity   80.0%;  Pred. No. 36;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          8 AGGCT 12


RESULT 65
CQ624605
LOCUS       CQ624605                  17 bp    DNA     linear   PAT 02-FEB-2004
DEFINITION  Sequence 9345 from Patent WO0192524.
ACCESSION   CQ624605
VERSION     CQ624605.1  GI:41674823
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
  TITLE     Myosin-like gene expressed in human heart and muscle
  JOURNAL   Patent: WO 0192524-A 9345 06-DEC-2001;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 17;
  Best Local Similarity   80.0%;  Pred. No. 36;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          7 AGGCT 11


RESULT 66
CQ624606
LOCUS       CQ624606                  17 bp    DNA     linear   PAT 02-FEB-2004
DEFINITION  Sequence 9346 from Patent WO0192524.
ACCESSION   CQ624606
VERSION     CQ624606.1  GI:41674824
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
  TITLE     Myosin-like gene expressed in human heart and muscle
  JOURNAL   Patent: WO 0192524-A 9346 06-DEC-2001;
```

```
          Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 17;
  Best Local Similarity   80.0%;  Pred. No. 36;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          6 AGGCT 10


RESULT 67
AR465667
LOCUS       AR465667                  17 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 9344 from patent US 6686188.
ACCESSION   AR465667
VERSION     AR465667.1  GI:42700724
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
  TITLE     Polynucleotide encoding a human myosin-like polypeptide expressed
            predominantly in heart and muscle
  JOURNAL   Patent: US 6686188-A 9344 03-FEB-2004;
            Amersham PLC; Buckinghamshire;
            GBX;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 17;
  Best Local Similarity   80.0%;  Pred. No. 36;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          8 AGGCT 12


RESULT 68
AR465668
LOCUS       AR465668                  17 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 9345 from patent US 6686188.
ACCESSION   AR465668
VERSION     AR465668.1  GI:42700725
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
  TITLE     Polynucleotide encoding a human myosin-like polypeptide expressed
            predominantly in heart and muscle
  JOURNAL   Patent: US 6686188-A 9345 03-FEB-2004;
            Amersham PLC; Buckinghamshire;
            GBX;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 17;
  Best Local Similarity   80.0%;  Pred. No. 36;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          7 AGGCT 11


RESULT 69
AR465669
LOCUS       AR465669                  17 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 9346 from patent US 6686188.
ACCESSION   AR465669
VERSION     AR465669.1  GI:42700726
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
  TITLE     Polynucleotide encoding a human myosin-like polypeptide expressed
            predominantly in heart and muscle
  JOURNAL   Patent: US 6686188-A 9346 03-FEB-2004;
            Amersham PLC; Buckinghamshire;
            GBX;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 17;
  Best Local Similarity   80.0%;  Pred. No. 36;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          6 AGGCT 10


RESULT 70
BD239234
LOCUS       BD239234                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD239234
VERSION     BD239234.1  GI:33049004
KEYWORDS    JP 2002534056-A/652.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 652 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/652
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
            19-JUN-1998 US    60/090080,19-JUN-1998 US    60/089833 PR
            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
```

```
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             16.0%;  Score 3.2;  DB 1;  Length 10;
  Best Local Similarity   62.5%;  Pred. No. 63;
  Matches    5;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 CTCCAGTC 12
              ||  || |
Db          2 CTGGAGCC 9


RESULT 71
AX623703
LOCUS       AX623703                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 744 from Patent WO02053774.
ACCESSION   AX623703
VERSION     AX623703.1  GI:28451644
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 744 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             16.0%;  Score 3.2;  DB 1;  Length 11;
  Best Local Similarity   62.5%;  Pred. No. 58;
  Matches    5;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 CTCCAGTC 12
              ||  || |
Db          3 CTGGAGAC 10


RESULT 72
AX631124
LOCUS       AX631124                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 8165 from Patent WO02053774.
ACCESSION   AX631124
VERSION     AX631124.1  GI:28459168
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 8165 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             16.0%;  Score 3.2;  DB 1;  Length 11;
  Best Local Similarity   62.5%;  Pred. No. 58;
  Matches    5;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 CTCCAGTC 12
              ||  || |
Db          3 CTGGAGAC 10


RESULT 73
I86909/c
LOCUS       I86909                    10 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 9 from patent US 5702926.
ACCESSION   I86909
VERSION     I86909.1  GI:3206627
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Fraiser,M.S. and Walker,G.Terrance.
  TITLE     Nicking of DNA using boronated nucleotides
  JOURNAL   Patent: US 5702926-A 9 30-DEC-1997;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             15.0%;  Score 3;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 65;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTG 3
              |||
Db          8 TTG 6


RESULT 74
BD065278/c
LOCUS       BD065278                  10 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Characterization of the yeast transcriptome.
ACCESSION   BD065278
VERSION     BD065278.1  GI:22610881
KEYWORDS    JP 2001509017-A/214.
SOURCE      Saccharomyces cerevisiae (baker's yeast)
  ORGANISM  Saccharomyces cerevisiae
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Characterization of the yeast transcriptome
  JOURNAL   Patent: JP 2001509017-A 214 10-JUL-2001;
            THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
COMMENT     OS   Saccharomyces cerevisiae (yeast)
            PN   JP 2001509017-A/214
            PD   10-JUL-2001
            PF   22-JAN-1998 JP 1998532117
            PR   23-JAN-1997 US    60/035917
            PI   VICTOR E VELCULESCU,BERT VOGELSTEIN,KENNETH W KINZLER PC
            C12N15/10,C12N15/31,C07K14/395,C12Q1/68,C12Q1/02 CC
            Characterization of the yeast transcriptome
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Saccharomyces cerevisiae (yeast)'.
```

```
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Saccharomyces cerevisiae"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:4932"

  Query Match             14.0%;  Score 2.8;  DB 1;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 67;
  Matches    4;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CTCCAG 10
              ||  ||
Db          7 CTGGAG 2


RESULT 75
BD161225/c
LOCUS       BD161225                  10 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Human activated Th1 and Th2 cell expression genes.
ACCESSION   BD161225
VERSION     BD161225.1  GI:27866983
KEYWORDS    JP 2002186482-A/47.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Nagai,S., Matsushima,K. and Hashimoto,S.
  TITLE     Human activated Th1 and Th2 cell expression genes
  JOURNAL   Patent: JP 2002186482-A 47 02-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002186482-A/47
            PD   02-JUL-2002
            PF   19-DEC-2000 JP 2000385816
            PI   SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
            C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC   Human
            activated Th1 and Th2 cell expression genes FH   Key
            Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             14.0%;  Score 2.8;  DB 1;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 67;
  Matches    4;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CTCCAG 10
              ||  ||
Db          9 CTGGAG 4


RESULT 76
E39559/c
LOCUS       E39559                    10 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Genes with human dendritic cell expression.
ACCESSION   E39559
VERSION     E39559.1  GI:18621650
KEYWORDS    JP 2000279181-A/92.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Hashimoto,S., Matsushima,K. and Suzuki,T.
  TITLE     Genes with human dendritic cell expression
  JOURNAL   Patent: JP 2000279181-A 92 10-OCT-2000;
            SCIENCE & TECH AGENCY
COMMENT     OS   Homo sapiens (human)
            PN   JP 2000279181-A/92
            PD   10-OCT-2000
            PF   01-APR-1999 JP 1999095481
            PR
            PI   SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
            C12N15/09,C07K14/475,C07K16/18,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             14.0%;  Score 2.8;  DB 1;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 67;
  Matches    4;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CTCCAG 10
              ||  ||
Db          9 CTGGAG 4


RESULT 77
AX152455/c
LOCUS       AX152455                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 370 from Patent WO0138577.
ACCESSION   AX152455
VERSION     AX152455.1  GI:14534106
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 370 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             14.0%;  Score 2.8;  DB 1;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 67;
  Matches    4;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CTCCAG 10
              ||  ||
Db          9 CTGGAG 4


RESULT 78
AX301660/c
LOCUS       AX301660                  10 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 374 from Patent WO0185941.
ACCESSION   AX301660
VERSION     AX301660.1  GI:17382743
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Versteeg,R. and Caron,H.N.
```

```
  TITLE     Myc targets
  JOURNAL   Patent: WO 0185941-A 374 15-NOV-2001;
            Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             14.0%;  Score 2.8;  DB 1;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 67;
  Matches    4;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CTCCAG 10
              ||  ||
Db          9 CTGGAG 4


RESULT 79
CQ787902/c
LOCUS       CQ787902                  8 bp    DNA     linear   PAT 24-MAR-2004
DEFINITION  Sequence 208 from Patent WO2004020664.
ACCESSION   CQ787902
VERSION     CQ787902.1  GI:45722860
KEYWORDS    .
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1
  AUTHORS   Geldermann,H., Preuss,S. and Han,Y.
  TITLE     Polymorphous microsatellite loci in genes for pre-diagnostic
            purposes
  JOURNAL   Patent: WO 2004020664-A 208 11-MAR-2004;
            Universitaet Hohenheim (DE)
FEATURES             Location/Qualifiers
     source          1. .8
                     /organism="Bos taurus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9913"
     satellite       1. .8
                     /note="R16, Allel H"
     repeat_unit     1
                     /note="Anzahl der Wiederholungen: 4"
     repeat_unit     3
                     /note="Anzahl der Wiederholungen: 13"
     repeat_unit     5
                     /note="Anzahl der Wiederholungen: 3"
     repeat_unit     8
                     /note="Anzahl der Wiederholungen: 4"

  Query Match             12.0%;  Score 2.4;  DB 1;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 98;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTC 12
              || |
Db          5 AGAC 2


RESULT 80
CS133813/c
LOCUS       CS133813                  9 bp    DNA     linear   PAT 02-AUG-2005
DEFINITION  Sequence 355 from Patent WO2005058479.
ACCESSION   CS133813
VERSION     CS133813.1  GI:71793362
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Morgan,B.
  TITLE     Methods for synthesis of encoded libraries
  JOURNAL   Patent: WO 2005058479-A 355 30-JUN-2005;
            Praecis Pharmaceuticals Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic construct"

  Query Match             12.0%;  Score 2.4;  DB 1;  Length 9;
  Best Local Similarity   75.0%;  Pred. No. 87;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 CCAG 10
              | ||
Db          8 CGAG 5


RESULT 81
CS133890
LOCUS       CS133890                  9 bp    DNA     linear   PAT 02-AUG-2005
DEFINITION  Sequence 432 from Patent WO2005058479.
ACCESSION   CS133890
VERSION     CS133890.1  GI:71793439
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Morgan,B.
  TITLE     Methods for synthesis of encoded libraries
  JOURNAL   Patent: WO 2005058479-A 432 30-JUN-2005;
            Praecis Pharmaceuticals Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic construct"

  Query Match             12.0%;  Score 2.4;  DB 1;  Length 9;
  Best Local Similarity   75.0%;  Pred. No. 87;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GTCT 6
              | ||
Db          6 GACT 9


RESULT 82
CS133996
LOCUS       CS133996                  9 bp    DNA     linear   PAT 02-AUG-2005
DEFINITION  Sequence 538 from Patent WO2005058479.
ACCESSION   CS133996
VERSION     CS133996.1  GI:71793545
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Morgan,B.
  TITLE     Methods for synthesis of encoded libraries
  JOURNAL   Patent: WO 2005058479-A 538 30-JUN-2005;
            Praecis Pharmaceuticals Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic construct"

  Query Match             12.0%;  Score 2.4;  DB 1;  Length 9;
```

```
  Best Local Similarity   75.0%;  Pred. No. 87;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 CCAG 10
              | ||
Db          1 CGAG 4


RESULT 83
A11620
LOCUS       A11620                    10 bp    DNA     linear   PAT 17-NOV-1993
DEFINITION  oligonucleotide 'M''.
ACCESSION   A11620
VERSION     A11620.1  GI:489366
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Ueda,I., Niwa,M., Saito,Y., Sato,S., Ono,H. and Kitaguchi,T.
  TITLE     59 Valine insulin-like growth factor I and process for production
            thereof
  JOURNAL   Patent: EP 0158892-A 116 23-OCT-1985;
            FUJISAWA PHARMACEUTICAL CO., LTD
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             12.0%;  Score 2.4;  DB 1;  Length 10;
  Best Local Similarity   75.0%;  Pred. No. 70;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTC 12
              || |
Db          3 AGAC 6


RESULT 84
A35162
LOCUS       A35162                    10 bp    DNA     linear   PAT 06-DEC-1996
DEFINITION  Synthetic IGF-I gene oligo.
ACCESSION   A35162
VERSION     A35162.1  GI:1926821
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Ueda,I., Niwa,M., Satoh,S., Saitoh,Y. and Kusunoki,C.
  TITLE     Process for production of isulin-like growth factor I and plasmid
            for production thereof
  JOURNAL   Patent: EP 0219814-A 112 29-APR-1987;
            FUJISAWA PHARMACEUTICAL CO., LTD
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             12.0%;  Score 2.4;  DB 1;  Length 10;
  Best Local Similarity   75.0%;  Pred. No. 70;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTC 12
              || |
Db          3 AGAC 6


RESULT 85
CQ836521
LOCUS       CQ836521                  11 bp    DNA     linear   PAT 29-JUL-2004
DEFINITION  Sequence 1579 from Patent WO2004059001.
ACCESSION   CQ836521
VERSION     CQ836521.1  GI:50836055
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
  TITLE     Method for determining markers of human facial skin
  JOURNAL   Patent: WO 2004059001-A 1579 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             11.0%;  Score 2.2;  DB 1;  Length 11;
  Best Local Similarity   57.1%;  Pred. No. 65;
  Matches    4;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          9 AGTCTCT 15
              ||   ||
Db          3 AGAAACT 9


RESULT 86
CS133889/c
LOCUS       CS133889                   9 bp    DNA     linear   PAT 02-AUG-2005
DEFINITION  Sequence 431 from Patent WO2005058479.
ACCESSION   CS133889
VERSION     CS133889.1  GI:71793438
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Morgan,B.
  TITLE     Methods for synthesis of encoded libraries
  JOURNAL   Patent: WO 2005058479-A 431 30-JUN-2005;
            Praecis Pharmaceuticals Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic construct"

  Query Match             10.0%;  Score 2;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 87;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 CG 18
              ||
Db          8 CG 7


RESULT 87
AR492617
LOCUS       AR492617                  10 bp    DNA     linear   PAT 15-MAY-2004
DEFINITION  Sequence 43 from patent US 6716974.
ACCESSION   AR492617
VERSION     AR492617.1  GI:47262128
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Maciag,T., Zimrin,A.B., Small,D.J. and Prudovsky,I.A.
```

```
  TITLE     Therapeutic and diagnostic methods and compositions based on
            jagged/notch proteins and nucleic acids
  JOURNAL   Patent: US 6716974-A 43 06-APR-2004;
            Maine Medical Center Research Institute; Scarborough, ME
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             10.0%;  Score 2;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 72;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 AG 10
              ||
Db          2 AG 3


RESULT 88
AX924254
LOCUS       AX924254                  11 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 39 from Patent EP1350841.
ACCESSION   AX924254
VERSION     AX924254.1  GI:40217178
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Schoenbrunner,N.J., Myers,T.W. and Gelfland,D.H.
  TITLE     Thermostable or thermoactive DNA polymerase with attenuated
            3'-5'exonuclease activity
  JOURNAL   Patent: EP 1350841-A 39 08-OCT-2003;
            Roche Diagnostics GmbH (DE) ; F. HOFFMANN-LA ROCHE AG (CH)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             10.0%;  Score 2;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 CG 18
              ||
Db          1 CG 2


Search completed: April 23, 2006, 11:37:56
Job time : 0.001 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 23, 2006, 11:47:44 ; Search time 0.001 Seconds
(without alignments)
13.200 Million cell updates/sec

Title: US-10-728-399-1
Perfect score: 20
Sequence: 1 ttgtctccagtctcttcgtt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 19 seqs, 330 residues

Total number of hits satisfying chosen parameters: 38

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : rnpbm.subdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	1	US-10-728-399-1	Sequence 1, Appli
	2	19	95.0	20	1	US-10-728-399-3	Sequence 3, Appli
	3	19	95.0	20	1	US-10-728-399-4	Sequence 4, Appli
	4	18	90.0	20	1	US-10-728-399-2	Sequence 2, Appli
	5	18	90.0	20	1	US-10-728-399-10	Sequence 10, Appl
	6	17	85.0	20	1	US-10-728-399-7	Sequence 7, Appli
	7	17	85.0	20	1	US-10-728-399-18	Sequence 18, Appl
	8	16	80.0	20	1	US-10-728-399-5	Sequence 5, Appli
	9	16	80.0	20	1	US-10-728-399-24	Sequence 24, Appl
c	10	13.8	69.0	17	1	US-09-866-108-9344	Sequence 9344, Ap
c	11	13.8	69.0	17	1	US-09-866-108-9345	Sequence 9345, Ap
c	12	13.8	69.0	17	1	US-09-866-108-9346	Sequence 9346, Ap
c	13	13.8	69.0	17	1	US-10-723-361-9344	Sequence 9344, Ap
c	14	13.8	69.0	17	1	US-10-723-361-9345	Sequence 9345, Ap
c	15	13.8	69.0	17	1	US-10-723-361-9346	Sequence 9346, Ap
c	16	10.4	52.0	13	1	US-10-257-017B-103673	Sequence 103673,
	17	10.4	52.0	13	1	US-10-257-017B-103674	Sequence 103674,
c	18	9	45.0	11	1	US-10-401-403-39	Sequence 39, Appl
c	19	9	45.0	11	1	US-10-450-797-1152	Sequence 1152, Ap
c	20	3.6	18.0	20	1	US-10-728-399-1	Sequence 1, Appli
c	21	3.6	18.0	20	1	US-10-728-399-3	Sequence 3, Appli
c	22	3.6	18.0	20	1	US-10-728-399-4	Sequence 4, Appli
c	23	3.6	18.0	20	1	US-10-728-399-2	Sequence 2, Appli
c	24	3.6	18.0	20	1	US-10-728-399-10	Sequence 10, Appl
c	25	3.6	18.0	20	1	US-10-728-399-18	Sequence 18, Appl
c	26	3.6	18.0	20	1	US-10-728-399-24	Sequence 24, Appl
	27	3.4	17.0	11	1	US-10-450-797-1152	Sequence 1152, Ap
	28	3.4	17.0	17	1	US-09-866-108-9344	Sequence 9344, Ap
	29	3.4	17.0	17	1	US-09-866-108-9345	Sequence 9345, Ap
	30	3.4	17.0	17	1	US-09-866-108-9346	Sequence 9346, Ap
	31	3.4	17.0	17	1	US-10-723-361-9344	Sequence 9344, Ap
	32	3.4	17.0	17	1	US-10-723-361-9345	Sequence 9345, Ap
	33	3.4	17.0	17	1	US-10-723-361-9346	Sequence 9346, Ap
c	34	3.4	17.0	20	1	US-10-728-399-7	Sequence 7, Appli
c	35	3.4	17.0	20	1	US-10-728-399-5	Sequence 5, Appli
	36	2.4	12.0	13	1	US-10-257-017B-103673	Sequence 103673,
c	37	2.4	12.0	13	1	US-10-257-017B-103674	Sequence 103674,
	38	2	10.0	11	1	US-10-401-403-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1
US-10-728-399-1
; Sequence 1, Application US/10728399
; Publication No. US20040132078A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Colca, Jerry
; TITLE OF INVENTION: ANTISENSE MODULATION OF mitoNEET EXPRESSION
; FILE REFERENCE: 01455_1
; CURRENT APPLICATION NUMBER: US/10/728,399
; CURRENT FILING DATE: 2003-12-05
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human mitoNEET antisense
US-10-728-399-1

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TTGTCTCCAGTCTCTTCGTT 20
              ||||||||||||||||||||
Db          1 TTGTCTCCAGTCTCTTCGTT 20
```

RESULT 2
US-10-728-399-3
; Sequence 3, Application US/10728399
; Publication No. US20040132078A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Colca, Jerry
; TITLE OF INVENTION: ANTISENSE MODULATION OF mitoNEET EXPRESSION
; FILE REFERENCE: 01455_1
; CURRENT APPLICATION NUMBER: US/10/728,399
; CURRENT FILING DATE: 2003-12-05
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human mitoNEET antisense
US-10-728-399-3

Query Match 95.0%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 TGTCTCCAGTCTCTTCGTT 20
              ||||||||||||||||||||
Db          1 TGTCTCCAGTCTCTTCGTT 19
```

RESULT 3
US-10-728-399-4
; Sequence 4, Application US/10728399

```
; Publication No. US20040132078A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Colca, Jerry
;  TITLE OF INVENTION: ANTISENSE MODULATION OF mitoNEET EXPRESSION
;  FILE REFERENCE: 01455_1
;  CURRENT APPLICATION NUMBER: US/10/728,399
;  CURRENT FILING DATE:  2003-12-05
;  NUMBER OF SEQ ID NOS: 627
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human mitoNEET antisense
US-10-728-399-4

  Query Match             95.0%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.4;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTGTCTCCAGTCTCTTCGT 19
              |||||||||||||||||||
Db          2 TTGTCTCCAGTCTCTTCGT 20


RESULT 4
US-10-728-399-2
; Sequence 2, Application US/10728399
; Publication No. US20040132078A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Colca, Jerry
;  TITLE OF INVENTION: ANTISENSE MODULATION OF mitoNEET EXPRESSION
;  FILE REFERENCE: 01455_1
;  CURRENT APPLICATION NUMBER: US/10/728,399
;  CURRENT FILING DATE:  2003-12-05
;  NUMBER OF SEQ ID NOS: 627
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human mitoNEET antisense
US-10-728-399-2

  Query Match             90.0%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.9;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAGTCTCTTCGTT 20
              ||||||||||||||||||
Db          1 GTCTCCAGTCTCTTCGTT 18


RESULT 5
US-10-728-399-10
; Sequence 10, Application US/10728399
; Publication No. US20040132078A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Colca, Jerry
;  TITLE OF INVENTION: ANTISENSE MODULATION OF mitoNEET EXPRESSION
;  FILE REFERENCE: 01455_1
;  CURRENT APPLICATION NUMBER: US/10/728,399
;  CURRENT FILING DATE:  2003-12-05
;  NUMBER OF SEQ ID NOS: 627
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human mitoNEET antisense
US-10-728-399-10

  Query Match             90.0%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.9;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTGTCTCCAGTCTCTTCG 18
              ||||||||||||||||||
Db          3 TTGTCTCCAGTCTCTTCG 20


RESULT 6
US-10-728-399-7
; Sequence 7, Application US/10728399
; Publication No. US20040132078A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Colca, Jerry
;  TITLE OF INVENTION: ANTISENSE MODULATION OF mitoNEET EXPRESSION
;  FILE REFERENCE: 01455_1
;  CURRENT APPLICATION NUMBER: US/10/728,399
;  CURRENT FILING DATE:  2003-12-05
;  NUMBER OF SEQ ID NOS: 627
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human mitoNEET antisense
US-10-728-399-7

  Query Match             85.0%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.5;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TCTCCAGTCTCTTCGTT 20
              |||||||||||||||||
Db          1 TCTCCAGTCTCTTCGTT 17


RESULT 7
US-10-728-399-18
; Sequence 18, Application US/10728399
; Publication No. US20040132078A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Colca, Jerry
;  TITLE OF INVENTION: ANTISENSE MODULATION OF mitoNEET EXPRESSION
;  FILE REFERENCE: 01455_1
;  CURRENT APPLICATION NUMBER: US/10/728,399
;  CURRENT FILING DATE:  2003-12-05
;  NUMBER OF SEQ ID NOS: 627
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human mitoNEET antisense
US-10-728-399-18

  Query Match             85.0%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.5;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTGTCTCCAGTCTCTTC 17
              |||||||||||||||||
Db          4 TTGTCTCCAGTCTCTTC 20
```

```
RESULT 8
US-10-728-399-5
; Sequence 5, Application US/10728399
; Publication No. US20040132078A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Colca, Jerry
;  TITLE OF INVENTION: ANTISENSE MODULATION OF mitoNEET EXPRESSION
;  FILE REFERENCE: 01455_1
;  CURRENT APPLICATION NUMBER: US/10/728,399
;  CURRENT FILING DATE:  2003-12-05
;  NUMBER OF SEQ ID NOS: 627
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human mitoNEET antisense
US-10-728-399-5

  Query Match             80.0%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.2;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CTCCAGTCTCTTCGTT 20
              ||||||||||||||||
Db          1 CTCCAGTCTCTTCGTT 16


RESULT 9
US-10-728-399-24
; Sequence 24, Application US/10728399
; Publication No. US20040132078A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Colca, Jerry
;  TITLE OF INVENTION: ANTISENSE MODULATION OF mitoNEET EXPRESSION
;  FILE REFERENCE: 01455_1
;  CURRENT APPLICATION NUMBER: US/10/728,399
;  CURRENT FILING DATE:  2003-12-05
;  NUMBER OF SEQ ID NOS: 627
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human mitoNEET antisense
US-10-728-399-24

  Query Match             80.0%;  Score 16;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.2;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTGTCTCCAGTCTCTT 16
              ||||||||||||||||
Db          5 TTGTCTCCAGTCTCTT 20


RESULT 10
US-09-866-108-9344/c
; Sequence 9344, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 9344
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-9344

  Query Match             69.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 7.6;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 TCTCCAGTCTCTTCGTT 20
              || |||| |||||||||
Db         17 TCCCCAGCCTCTTCGTT 1


RESULT 11
US-09-866-108-9345/c
; Sequence 9345, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
```

```
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 9345
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-9345

  Query Match             69.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 7.6;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAGTCTCTTCGT 19
              ||| |||| ||||||||
Db         17 GTCCCCAGCCTCTTCGT 1


RESULT 12
US-09-866-108-9346/c
; Sequence 9346, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 9346
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-9346

  Query Match             69.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 7.6;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TGTCTCCAGTCTCTTCG 18
              |||| |||| |||||||
Db         17 TGTCCCCAGCCTCTTCG 1


RESULT 13
US-10-723-361-9344/c
; Sequence 9344, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
;  FILE REFERENCE: PB0105
;  CURRENT APPLICATION NUMBER: US/10/723,361
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: US 09/866,108
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 15755
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 9344
;   LENGTH: 17
;   TYPE: DNA
```

```
;   ORGANISM: Homo sapiens
US-10-723-361-9344

  Query Match             69.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 7.6;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 TCTCCAGTCTCTTCGTT 20
              || |||| |||||||||
Db         17 TCCCCAGCCTCTTCGTT 1


RESULT 14
US-10-723-361-9345/c
; Sequence 9345, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
;  FILE REFERENCE: PB0105
;  CURRENT APPLICATION NUMBER: US/10/723,361
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: US 09/866,108
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 15755
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 9345
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-723-361-9345

  Query Match             69.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 7.6;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAGTCTCTTCGT 19
              ||| |||| ||||||||
Db         17 GTCCCCAGCCTCTTCGT 1


RESULT 15
US-10-723-361-9346/c
; Sequence 9346, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
;  FILE REFERENCE: PB0105
;  CURRENT APPLICATION NUMBER: US/10/723,361
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: US 09/866,108
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 15755
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 9346
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-723-361-9346

  Query Match             69.0%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 7.6;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 TGTCTCCAGTCTCTTCG 18
              |||| |||| |||||||
Db         17 TGTCCCCAGCCTCTTCG 1


RESULT 16
US-10-257-017B-103673/c
; Sequence 103673, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
;  TITLE OF INVENTION:  methylations
;  FILE REFERENCE: E01/1193/WO
;  CURRENT APPLICATION NUMBER: US/10/257,017B
;  CURRENT FILING DATE:  2002-10-07
;  PRIOR APPLICATION NUMBER: DE 10019173.8
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 103673
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0025934
US-10-257-017B-103673

  Query Match             52.0%;  Score 10.4;  DB 1;  Length 13;
  Best Local Similarity   91.7%;  Pred. No. 18;
```

```
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCTCCAGTCTCT 15
              ||||| ||||||
Db         13 TCTCCCGTCTCT 2


RESULT 17
US-10-257-017B-103674
; Sequence 103674, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
;  TITLE OF INVENTION:  methylations
;  FILE REFERENCE: E01/1193/WO
;  CURRENT APPLICATION NUMBER: US/10/257,017B
;  CURRENT FILING DATE:  2002-10-07
;  PRIOR APPLICATION NUMBER: DE 10019173.8
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 103674
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0025934
US-10-257-017B-103674

  Query Match             52.0%;  Score 10.4;  DB 1;  Length 13;
  Best Local Similarity   91.7%;  Pred. No. 18;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCTCCAGTCTCT 15
              ||||| ||||||
Db          1 TCTCCCGTCTCT 12


RESULT 18
US-10-401-403-39/c
; Sequence 39, Application US/10401403
; Publication No. US20040005599A1
; GENERAL INFORMATION:
;  APPLICANT: Schoenbrunner, Nancy
;  APPLICANT:  Myers, Thomas
;  APPLICANT:  Gelfand, David
;  TITLE OF INVENTION: THERMOSTABLE OR THERMOACTIVE DNA POLYMERASE MOLECULES
;  TITLE OF INVENTION:  WITH ATTENUATED 3'-5' EXONUCLEASE ACTIVITY
;  FILE REFERENCE: 21314-US1
;  CURRENT APPLICATION NUMBER: US/10/401,403
;  CURRENT FILING DATE:  2003-03-26
;  PRIOR APPLICATION NUMBER: US 60/369,815
;  PRIOR FILING DATE: 2002-04-02
;  NUMBER OF SEQ ID NOS: 203
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Primer
US-10-401-403-39

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 TCTCTTCGT 19
              |||||||||
Db         11 TCTCTTCGT 3


RESULT 19
US-10-450-797-1152/c
; Sequence 1152, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
;  APPLICANT: Petersohn, Dirk
;  APPLICANT:  Conradt, Marcus
;  APPLICANT:  Hofmann, Kay
;  TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
;  FILE REFERENCE: HENK-0041
;  CURRENT APPLICATION NUMBER: US/10/450,797
;  CURRENT FILING DATE:  2003-12-04
;  PRIOR APPLICATION NUMBER: PCT/EP01/15178
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: DE 101 00 121.5
;  PRIOR FILING DATE: 2001-01-03
;  NUMBER OF SEQ ID NOS: 1435
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1152
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-450-797-1152

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 AGTCTCTTC 17
              |||||||||
Db         10 AGTCTCTTC 2


RESULT 20
US-10-728-399-1/c
; Sequence 1, Application US/10728399
; Publication No. US20040132078A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Colca, Jerry
;  TITLE OF INVENTION: ANTISENSE MODULATION OF mitoNEET EXPRESSION
;  FILE REFERENCE: 01455_1
;  CURRENT APPLICATION NUMBER: US/10/728,399
;  CURRENT FILING DATE:  2003-12-05
;  NUMBER OF SEQ ID NOS: 627
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human mitoNEET antisense
US-10-728-399-1

  Query Match             18.0%;  Score 3.6;  DB 1;  Length 20;
  Best Local Similarity   60.0%;  Pred. No. 27;
  Matches    6;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAGTC 12
              | ||  || |
Db         12 GACTGGAGAC 3


RESULT 21
US-10-728-399-3/c
; Sequence 3, Application US/10728399
; Publication No. US20040132078A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Colca, Jerry
;  TITLE OF INVENTION: ANTISENSE MODULATION OF mitoNEET EXPRESSION
;  FILE REFERENCE: 01455_1
```

```
;  CURRENT APPLICATION NUMBER: US/10/728,399
;  CURRENT FILING DATE:  2003-12-05
;  NUMBER OF SEQ ID NOS: 627
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human mitoNEET antisense
US-10-728-399-3

  Query Match             18.0%;  Score 3.6;  DB 1;  Length 20;
  Best Local Similarity   60.0%;  Pred. No. 27;
  Matches    6;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAGTC 12
              | ||  || |
Db         11 GACTGGAGAC 2


RESULT 22
US-10-728-399-4/c
; Sequence 4, Application US/10728399
; Publication No. US20040132078A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Colca, Jerry
;  TITLE OF INVENTION: ANTISENSE MODULATION OF mitoNEET EXPRESSION
;  FILE REFERENCE: 01455_1
;  CURRENT APPLICATION NUMBER: US/10/728,399
;  CURRENT FILING DATE:  2003-12-05
;  NUMBER OF SEQ ID NOS: 627
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human mitoNEET antisense
US-10-728-399-4

  Query Match             18.0%;  Score 3.6;  DB 1;  Length 20;
  Best Local Similarity   60.0%;  Pred. No. 27;
  Matches    6;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAGTC 12
              | ||  || |
Db         13 GACTGGAGAC 4


RESULT 23
US-10-728-399-2/c
; Sequence 2, Application US/10728399
; Publication No. US20040132078A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Colca, Jerry
;  TITLE OF INVENTION: ANTISENSE MODULATION OF mitoNEET EXPRESSION
;  FILE REFERENCE: 01455_1
;  CURRENT APPLICATION NUMBER: US/10/728,399
;  CURRENT FILING DATE:  2003-12-05
;  NUMBER OF SEQ ID NOS: 627
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human mitoNEET antisense
US-10-728-399-2

  Query Match             18.0%;  Score 3.6;  DB 1;  Length 20;
  Best Local Similarity   60.0%;  Pred. No. 27;
  Matches    6;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAGTC 12
              | ||  || |
Db         10 GACTGGAGAC 1


RESULT 24
US-10-728-399-10/c
; Sequence 10, Application US/10728399
; Publication No. US20040132078A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Colca, Jerry
;  TITLE OF INVENTION: ANTISENSE MODULATION OF mitoNEET EXPRESSION
;  FILE REFERENCE: 01455_1
;  CURRENT APPLICATION NUMBER: US/10/728,399
;  CURRENT FILING DATE:  2003-12-05
;  NUMBER OF SEQ ID NOS: 627
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human mitoNEET antisense
US-10-728-399-10

  Query Match             18.0%;  Score 3.6;  DB 1;  Length 20;
  Best Local Similarity   60.0%;  Pred. No. 27;
  Matches    6;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAGTC 12
              | ||  || |
Db         14 GACTGGAGAC 5


RESULT 25
US-10-728-399-18/c
; Sequence 18, Application US/10728399
; Publication No. US20040132078A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Colca, Jerry
;  TITLE OF INVENTION: ANTISENSE MODULATION OF mitoNEET EXPRESSION
;  FILE REFERENCE: 01455_1
;  CURRENT APPLICATION NUMBER: US/10/728,399
;  CURRENT FILING DATE:  2003-12-05
;  NUMBER OF SEQ ID NOS: 627
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human mitoNEET antisense
US-10-728-399-18

  Query Match             18.0%;  Score 3.6;  DB 1;  Length 20;
  Best Local Similarity   60.0%;  Pred. No. 27;
  Matches    6;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAGTC 12
              | ||  || |
Db         15 GACTGGAGAC 6


RESULT 26
US-10-728-399-24/c
; Sequence 24, Application US/10728399
; Publication No. US20040132078A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Colca, Jerry
;  TITLE OF INVENTION: ANTISENSE MODULATION OF mitoNEET EXPRESSION
;  FILE REFERENCE: 01455_1
;  CURRENT APPLICATION NUMBER: US/10/728,399
;  CURRENT FILING DATE:  2003-12-05
;  NUMBER OF SEQ ID NOS: 627
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human mitoNEET antisense
US-10-728-399-24

  Query Match             18.0%;  Score 3.6;  DB 1;  Length 20;
  Best Local Similarity   60.0%;  Pred. No. 27;
  Matches    6;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAGTC 12
              | ||  || |
Db         16 GACTGGAGAC 7


RESULT 27
US-10-450-797-1152
; Sequence 1152, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
;  APPLICANT: Petersohn, Dirk
;  APPLICANT:  Conradt, Marcus
;  APPLICANT:  Hofmann, Kay
;  TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
;  FILE REFERENCE: HENK-0041
;  CURRENT APPLICATION NUMBER: US/10/450,797
;  CURRENT FILING DATE:  2003-12-04
;  PRIOR APPLICATION NUMBER: PCT/EP01/15178
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: DE 101 00 121.5
;  PRIOR FILING DATE: 2001-01-03
;  NUMBER OF SEQ ID NOS: 1435
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1152
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-450-797-1152

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 11;
  Best Local Similarity   80.0%;  Pred. No. 51;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          6 AGACT 10


RESULT 28
US-09-866-108-9344
; Sequence 9344, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 9344
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-9344

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 17;
  Best Local Similarity   80.0%;  Pred. No. 33;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          8 AGGCT 12


RESULT 29
US-09-866-108-9345
; Sequence 9345, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
```

```
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 9345
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-9345

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 17;
  Best Local Similarity   80.0%;  Pred. No. 33;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          7 AGGCT 11


RESULT 30
US-09-866-108-9346
; Sequence 9346, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 60/266,860
;  PRIOR FILING DATE: 2001-02-05
;  NUMBER OF SEQ ID NOS: 15752
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 9346
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108-9346

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 17;
  Best Local Similarity   80.0%;  Pred. No. 33;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          6 AGGCT 10


RESULT 31
US-10-723-361-9344
; Sequence 9344, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
;  FILE REFERENCE: PB0105
;  CURRENT APPLICATION NUMBER: US/10/723,361
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: US 09/866,108
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 15755
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 9344
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-723-361-9344
```

```
  Query Match             17.0%;  Score 3.4;  DB 1;  Length 17;
  Best Local Similarity   80.0%;  Pred. No. 33;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          8 AGGCT 12


RESULT 32
US-10-723-361-9345
; Sequence 9345, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
;  FILE REFERENCE: PB0105
;  CURRENT APPLICATION NUMBER: US/10/723,361
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: US 09/866,108
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 15755
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 9345
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-723-361-9345

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 17;
  Best Local Similarity   80.0%;  Pred. No. 33;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          7 AGGCT 11


RESULT 33
US-10-723-361-9346
; Sequence 9346, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
;  FILE REFERENCE: PB0105
;  CURRENT APPLICATION NUMBER: US/10/723,361
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: US 09/866,108
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 15755
;  SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 9346
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-723-361-9346

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 17;
  Best Local Similarity   80.0%;  Pred. No. 33;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          6 AGGCT 10


RESULT 34
US-10-728-399-7/c
; Sequence 7, Application US/10728399
; Publication No. US20040132078A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Colca, Jerry
;  TITLE OF INVENTION: ANTISENSE MODULATION OF mitoNEET EXPRESSION
;  FILE REFERENCE: 01455_1
;  CURRENT APPLICATION NUMBER: US/10/728,399
;  CURRENT FILING DATE:  2003-12-05
;  NUMBER OF SEQ ID NOS: 627
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human mitoNEET antisense
US-10-728-399-7

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 28;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db         10 AGACT 6
```

```
RESULT 35
US-10-728-399-5/c
; Sequence 5, Application US/10728399
; Publication No. US20040132078A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia Corp.
;  APPLICANT:  Colca, Jerry
;  TITLE OF INVENTION: ANTISENSE MODULATION OF mitoNEET EXPRESSION
;  FILE REFERENCE: 01455_1
;  CURRENT APPLICATION NUMBER: US/10/728,399
;  CURRENT FILING DATE:  2003-12-05
;  NUMBER OF SEQ ID NOS: 627
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: human mitoNEET antisense
US-10-728-399-5

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 20;
  Best Local Similarity   80.0%;  Pred. No. 28;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          9 AGACT 5


RESULT 36
US-10-257-017B-103673
; Sequence 103673, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
;  TITLE OF INVENTION:  methylations
;  FILE REFERENCE: E01/1193/WO
;  CURRENT APPLICATION NUMBER: US/10/257,017B
;  CURRENT FILING DATE:  2002-10-07
;  PRIOR APPLICATION NUMBER: DE 10019173.8
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 103673
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0025934
US-10-257-017B-103673

  Query Match             12.0%;  Score 2.4;  DB 1;  Length 13;
  Best Local Similarity   75.0%;  Pred. No. 46;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTC 12
              || |
Db          4 AGAC 7


RESULT 37
US-10-257-017B-103674/c
; Sequence 103674, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
;  TITLE OF INVENTION:  methylations
;  FILE REFERENCE: E01/1193/WO
;  CURRENT APPLICATION NUMBER: US/10/257,017B
;  CURRENT FILING DATE:  2002-10-07
;  PRIOR APPLICATION NUMBER: DE 10019173.8
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 103674
;   LENGTH: 13
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0025934
US-10-257-017B-103674

  Query Match             12.0%;  Score 2.4;  DB 1;  Length 13;
  Best Local Similarity   75.0%;  Pred. No. 46;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTC 12
              || |
Db         10 AGAC 7


RESULT 38
US-10-401-403-39
; Sequence 39, Application US/10401403
; Publication No. US20040005599A1
; GENERAL INFORMATION:
;  APPLICANT: Schoenbrunner, Nancy
;  APPLICANT:  Myers, Thomas
;  APPLICANT:  Gelfand, David
;  TITLE OF INVENTION: THERMOSTABLE OR THERMOACTIVE DNA POLYMERASE MOLECULES
;  TITLE OF INVENTION:  WITH ATTENUATED 3'-5' EXONUCLEASE ACTIVITY
;  FILE REFERENCE: 21314-US1
;  CURRENT APPLICATION NUMBER: US/10/401,403
;  CURRENT FILING DATE:  2003-03-26
;  PRIOR APPLICATION NUMBER: US 60/369,815
;  PRIOR FILING DATE: 2002-04-02
;  NUMBER OF SEQ ID NOS: 203
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Primer
US-10-401-403-39

  Query Match             10.0%;  Score 2;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 55;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 CG 18
              ||
Db          1 CG 2


Search completed: April 23, 2006, 11:47:45
Job time : 0.001 secs
```

THIS PAGE LEFT BLANK

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 23, 2006, 11:49:35 ; Search time 0.001 Seconds
(without alignments)
3.040 Million cell updates/sec

Title: US-10-728-399-1
Perfect score: 20
Sequence: 1 ttgtctccagtctcttcgtt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 4 seqs, 76 residues

Total number of hits satisfying chosen parameters: 8

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : rnpbn.subdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	18	90.0	19	1	US-11-101-244-1102924	Sequence 1102924,
c	2	18	90.0	19	1	US-11-083-784-1102924	Sequence 1102924,
c	3	17	85.0	19	1	US-11-101-244-1102943	Sequence 1102943,
c	4	17	85.0	19	1	US-11-083-784-1102943	Sequence 1102943,
	5	3.6	18.0	19	1	US-11-101-244-1102924	Sequence 1102924,
	6	3.6	18.0	19	1	US-11-083-784-1102924	Sequence 1102924,
	7	3.6	18.0	19	1	US-11-101-244-1102943	Sequence 1102943,
	8	3.6	18.0	19	1	US-11-083-784-1102943	Sequence 1102943,

ALIGNMENTS

RESULT 1
US-11-101-244-1102924/c
; Sequence 1102924, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1102924
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1102924

Query Match 90.0%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TTGTCTCCAGTCTCTTCG 18
              ||||||||||||||||||
Db         18 TTGTCTCCAGTCTCTTCG 1
```

RESULT 2
US-11-083-784-1102924/c
; Sequence 1102924, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1102924
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1102924

Query Match 90.0%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TTGTCTCCAGTCTCTTCG 18
              ||||||||||||||||||
Db         18 TTGTCTCCAGTCTCTTCG 1
```

RESULT 3
US-11-101-244-1102943/c
; Sequence 1102943, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14

```
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1102943
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-1102943

  Query Match             85.0%;  Score 17;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTGTCTCCAGTCTCTTC 17
              |||||||||||||||||
Db         17 TTGTCTCCAGTCTCTTC 1


RESULT 4
US-11-083-784-1102943/c
; Sequence 1102943, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1102943
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-1102943

  Query Match             85.0%;  Score 17;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTGTCTCCAGTCTCTTC 17
              |||||||||||||||||
Db         17 TTGTCTCCAGTCTCTTC 1


RESULT 5
US-11-101-244-1102924
; Sequence 1102924, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1102924
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-1102924

  Query Match             18.0%;  Score 3.6;  DB 1;  Length 19;
  Best Local Similarity   50.0%;  Pred. No. 6.9;
  Matches    5;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAGTC 12
              | |:  || |
Db          7 GACUGGAGAC 16


RESULT 6
US-11-083-784-1102924
; Sequence 1102924, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1102924
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-1102924

  Query Match             18.0%;  Score 3.6;  DB 1;  Length 19;
  Best Local Similarity   50.0%;  Pred. No. 6.9;
  Matches    5;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAGTC 12
              | |:  || |
Db          7 GACUGGAGAC 16


RESULT 7
US-11-101-244-1102943
; Sequence 1102943, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
```

```
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1102943
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-1102943

  Query Match             18.0%;  Score 3.6;  DB 1;  Length 19;
  Best Local Similarity   50.0%;  Pred. No. 6.9;
  Matches    5;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAGTC 12
              | |:  || |
Db          6 GACUGGAGAC 15


RESULT 8
US-11-083-784-1102943
; Sequence 1102943, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1102943
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-1102943

  Query Match             18.0%;  Score 3.6;  DB 1;  Length 19;
  Best Local Similarity   50.0%;  Pred. No. 6.9;
  Matches    5;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GTCTCCAGTC 12
              | |:  || |
Db          6 GACUGGAGAC 15


Search completed: April 23, 2006, 11:49:35
Job time : 0.001 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 23, 2006, 11:51:51 ; Search time 0.001 Seconds
(without alignments)
0.680 Million cell updates/sec

Title: US-10-728-399-1
Perfect score: 20
Sequence: 1 ttgtctccagtctcttcgtt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 2 seqs, 17 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : rst.subdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	9	45.0	9	1	CF313414	ACCESSION:CF313414
	2	6.4	32.0	8	1	CV933313	ACCESSION:CV933313
	3	3.4	17.0	9	1	CF313414	ACCESSION:CF313414
c	4	2.4	12.0	8	1	CV933313	ACCESSION:CV933313

ALIGNMENTS

RESULT 1
CF313414/c
LOCUS CF313414 9 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--01-I15.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--01-I15, mRNA sequence.
ACCESSION CF313414
VERSION CF313414.1 GI:33685175
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 9)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .9
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--01-I15"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 45.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CTCCAGTCT 13
|||||||||
Db 9 CTCCAGTCT 1

RESULT 2
CV933313
LOCUS CV933313 8 bp mRNA linear EST 25-JAN-2005
DEFINITION PMpcm_0658 mating of 88069 (A1) and 618 (A2) Phytophthora infestans cDNA, mRNA sequence.
ACCESSION CV933313
VERSION CV933313.1 GI:58122928
KEYWORDS EST.
SOURCE Phytophthora infestans (potato late blight agent)
ORGANISM Phytophthora infestans
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae; Phytophthora.
REFERENCE 1 (bases 1 to 8)
AUTHORS Randall,T., Dwyer,R.A., Huitema,E., Beyer,K., Cvitanich,C., Kelkar,H., Fong,A.M., Gates,K., Roberts,S., Yatzkan,E., Gaffney,T., Law,M., Testa,A., Torto-Alalibo,A., Zhang,M., Zheng,L., Mueller,E., Windass,J., Binder,A., Birch,P.R.J., Gisi,U., Govers,F., Gow,N.A., Mauch,F., van West,P., Waugh,M.E., Yu,J., Boller,T., Kamoun,S., Lam,S.T. and Judelson, H.S.
TITLE Large-scale gene discovery in the oomycete Phytophthora infestans reveals likely components of phytopathogenicity shared with true fungi
JOURNAL Mol. Plant-Microbe Interact. 18 (3), 229-243 (2005)
PUBMED 15782637
COMMENT Contact: Judelson HS
Department of Plant Pathology
University of California
Webber Hall, Riverside, CA 92521, USA
Tel: 909 787 4199
Fax: 909 787 4294
Email: howard.judelson@ucr.edu.
FEATURES Location/Qualifiers
source 1. .8
/organism="Phytophthora infestans"
/mol_type="mRNA"
/strain="88069 and 618"
/db_xref="taxon:4787"
/sex="A1 and A2"
/clone_lib="mating of 88069 (A1) and 618 (A2)"
/note="Vector: pSPORT1"

Query Match 32.0%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 TTGTCTCC 8
              ||||| ||
Db          1 TTGTCACC 8


RESULT 3
CF313414
LOCUS       CF313414                  9 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--01-I15.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--01-I15, mRNA sequence.
ACCESSION   CF313414
VERSION     CF313414.1  GI:33685175
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 9)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="HD--01-I15"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."

  Query Match             17.0%;  Score 3.4;  DB 1;  Length 9;
  Best Local Similarity   80.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 AGTCT 13
              || ||
Db          1 AGACT 5


RESULT 4
CV933313/c
LOCUS       CV933313                  8 bp    mRNA    linear   EST 25-JAN-2005
DEFINITION  PMpcm_0658 mating of 88069 (A1) and 618 (A2) Phytophthora infestans
            cDNA, mRNA sequence.
ACCESSION   CV933313
VERSION     CV933313.1  GI:58122928
KEYWORDS    EST.
SOURCE      Phytophthora infestans (potato late blight agent)
  ORGANISM  Phytophthora infestans
            Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
            Phytophthora.
REFERENCE   1  (bases 1 to 8)
  AUTHORS   Randall,T., Dwyer,R.A., Huitema,E., Beyer,K., Cvitanich,C.,
            Kelkar,H., Fong,A.M., Gates,K., Roberts,S., Yatzkan,E., Gaffney,T.,
            Law,M., Testa,A., Torto-Alalibo,A., Zhang,M., Zheng,L., Mueller,E.,
            Windass,J., Binder,A., Birch,P.R.J., Gisi,U., Govers,F., Gow,N.A.,
            Mauch,F., van West,P., Waugh,M.E., Yu,J., Boller,T., Kamoun,S.,
            Lam,S.T. and Judelson, H.S.
  TITLE     Large-scale gene discovery in the oomycete Phytophthora infestans
            reveals likely components of phytopathogenicity shared with true
            fungi
  JOURNAL   Mol. Plant-Microbe Interact. 18 (3), 229-243 (2005)
  PUBMED    15782637
COMMENT     Contact: Judelson HS
            Department of Plant Pathology
            University of California
            Webber Hall, Riverside, CA 92521, USA
            Tel: 909 787 4199
            Fax: 909 787 4294
            Email: howard.judelson@ucr.edu.
FEATURES             Location/Qualifiers
     source          1. .8
                     /organism="Phytophthora infestans"
                     /mol_type="mRNA"
                     /strain="88069 and 618"
                     /db_xref="taxon:4787"
                     /sex="A1 and A2"
                     /clone_lib="mating of 88069 (A1) and 618 (A2)"
                     /note="Vector: pSPORT1"

  Query Match             12.0%;  Score 2.4;  DB 1;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TGTC 5
              || |
Db          6 TGAC 3


Search completed: April 23, 2006, 11:51:51
Job time : 0.001 secs
```